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Papaya leaf-distortion mosaic potyvirus
Papaya leaf-distortion mosaic potyvirus
Viruses; seRNA positive-strand viruses, no DNA stage; Potyviridae;
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The complete nucleotide sequence of Papaya leaf distortion mosaic
virus RNA: isolate variability and the origin of PLDMV
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Submitted (15-JUL-2002) Tetsuo Maoka, National Agricultural
Research Center for Hokkaido Region, Plant Virology Lab.;
Hitsujigaoka 1, Toyohira, Sapporo 0628555, Japan
(E-mail:maokat@æffcc.go.jp, URL:http://cryo.naro.affrc.go.jp/,
Tel:81-11-857-9278, Fax:81-11-859-2178)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Papaya leaf-distortion mosaic potyvirus genomic RNA, complete genome, strain:P.
AB088221.1 GI:33235542
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    10153 | Appaya leaf-distortion mosaic potyvirus | /organism="Papaya leaf-distortion mosaic potyvirus | /moi_type="genomic RNA" | /strain="p"

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Arch. Virol. 141 (1), 197-204 (1996)
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/db_xref="taxon:46917"
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AB016500 Japanese
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AB093597 Turnip mo
AB09359 Turnip mo
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AJ1341 Plum pox vi
AY184478 Plum pox vi
AY1840 Potato vi
V09851 Plum pox po
AB093616 Turnip mo
AB093612 Turnip mo
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Copyright (c) 1993 - 2005 Compugen Ltd.
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LSSKGAVLMLEPTRPLAENVSRQLRQHPFYANPTLRWRGMSSFGSSNICIMTSGFAFN
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/clone="P140"
/lab_host="Cucumber:Cucumis metuliferus"
/country="Japan:Okinawa, Ishigaki"
/note="contig of clone:P140, P16K111, C164, NIa41, NIb99,
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Best Local Similarity 73.0%; Pred. No. 0;
Matches 7409; Conservative 2744; Mismatches
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6061 AAGAATTTCAAAATTTCTAAATCTGAGAGGTAAGTGGAATAAGTCACTAATTACACGTG 6120 6122 AUAUCUUAGUUUAGGUGGUCACUAUUGGUGGUUUCUGGAUGAUUAUGGGAUAAGUUCA 6181	6302 AUDACUUUGGAUCGCCAUACGUCAAGAGGGCCAGUAAGGCCAGAAGAGGGAAUGG 6361 :: :: :		CGGCAAUAGCAGGGUUUCCUGAGAAGGAGUUUUUUCCGACAAACGGACAAAGGAUAUG 	6781 GTGTGAAGGGATTGCGCGATTACAATGGTGTAGCCGCTATTTGCCAACTCACAACA 6840 6842 ACUCAAAUGGUCCCCCCAACUUAUGGGUUGGCUUGGCUCAUACAUCAUAGUA 6901 [
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00,C12NS/00
CC Full-length genome RNA of papaya leaf distortion mosaic virus
FH Key Location/Qualifiers
FT CDS Location/Qualifiers
OS Papaya leaf-distortion mosaic virus
PN JP 2002238574-A/1
PD 27-AUG-2002
PP 16-FEB-2001 JP 2001040523
PI TETSUO MAOKA, TATSUJI HATAYA
PC C12N15/09, A01H1/00, C12N5/10, C12N9/50, C12P21/02, C12Q1/68, C12N15/ PC
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                                                 UGAUGCAAGGGAAGAACAAAUCGAAUACCCCCUUCAACCAAUAGUGGAAAACGCAAAAC
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TITLE
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BD171712
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Db 4022 AGAAAATTATAGCATTTGTTATGATGATGATTTTTGACTCAGAGAAAAGTGATT 4082 GUGUAUAAAGACACAGAAAUUGCGAAAUCUCGUUGCCACAUGUCGUCGUCG 1 1 1 1 1 1 1 1 1	4262 4262 4322 4322	4382 4382 4442 4442	0y 4502 UCCACGACAGUGAGACACACCCUUUN GGAACCCCAUGAGAGACACACACACACACACACACACACA	Qy 4622 UUGCAAAUAAUCCUCUAAAAUUAAGUGAUUUUGAAUUUGUGAUAAUAGUGUCACG :: : : : : bb 4622 TTGCAATAATCCTCTAAAATTAAGTGATTTTGAATTTGTGATAATAGATGATCTCACG Qy 4682 UCCUAGAUAGCAACGCUAUGGCAUUCGUGUGUCUUCUCAAAGAACACAACUAGAUGGCA bb 4682 TCCTAGATAGCAACGCTATGGCATTCGTGTGTCTTCTCAAAGAACACAACTATGATGGCA	Oy 4742 AACUAUUGAAAGUGUCAGCCACACCACAGGCCGUGAAUGUGAAUUCCACACACA	Oy 4862 CUGGGUCUGCACGAGAUGUAAUCAAUAAGGGAGACAACAUUUAGUGUAGUUGCUAGUU	Db 4922 ACAATGAGGTGATCATCAAAAATGCTCGGAGATAAAGGCTATTTAGTGACTGAAAA Qy 4982 UCGAUGGGCGUACCAUGAAAAUUGGUUCGACCACAUAGUUACUAAAGGGAGUAGCCAGA Db 4982 TCGATGGGCGTACCATGAAAATTGGTTGGACGACTAGTTACTAAAGGGAGTAGCCAGA	
	3122 TAGCTTTAAAGTACTGGATGAGCAAGCAACAGTCTGTCGCTGCTTTATTTGCAATGATCG 3181 3182 AUGGACUAGCUGCAAAAGUAACAGUUGCUCAAACAUUGAAUGAGCGAGAGCUAAUACUUG 3241 3182 ATGGACTGCTGCAAAAGTAACAGTTGCTCAAACATTGGAGAGAGA	3302 ACCAACCGGGGUUCUUCAACUACAGGUCAUGGCAAAUCGUAGAGACAUGAAUUCCACUC 3361 3302 ACCAACCGGGGTTCTTCAACTACAGGTCATGGCAAATCGTAGAGACATGAATTCCACTC 3361 3362 UUGAUCUCGCCGGAUUCAGGAUUACAAUCUGAAGAUAGUAUGGAUGG	GUUAUCUCAUGGAAUUAGAGGAUUCGUGGAACGACUUAAAGUGGUUGGAAAAAUUACAAG 3 -:- - - - - - - - - - - - - - - - -	CUACCGAUUNAGGCGGUCGAUAUCCAGUALGGAAAGAGCAGUUAUAAACGGGAUGAAGGCGGGGUCGAUGAAGGCGGGGGGGG	3602 AACCTGTCAAGAAATCTTGTGTAAAAGCAAGAGATACTTGTAAGGAAGTAATCATCAATA 3661 3662 CAACAUCCUGACUUUCGGGCAACAUUUUCUUGUGUAGGUGGUGCUUGCU	722 TGAAGTTTATAAACATGCTTATAGTTATAAGTTTGATTCTCAGCATTGGCATTCAGCTA 3 722 AUUCUAUAUCGUUCGACUAUGCACAAAUGAAGAAAGGAAAAGCAGGUGAAUAUCGAGAAAAG 782 ATTCTATATCGTTCGACTATGCACAAATGAAGAGAAAAGAAAAGCAGGTGAATATCGAGAAAAG 3	3942 TTCTGATGAATTTTAGTGGCCCTTCATAGGAGGAGAAAGGATGAAATCAATC	AUAAAGAAUUGCAAGAAGAAGUUGAUCAUCAAGCUAAGGGCAAAGGUGAACAAAACUUGG 40 - :

	6422 UUAGAUACAUAGAUCCCAUAACUGGAGCAACGGGGAUGAGAGUCCUUUGACAGAUGUGG 6481 :: : : : : :	6542 AUAGGCAACACUUAAAUAAACCAGGUUUGACAGCAUACUUAGUUAAGGACGGGGUUA 6601	6662 CGACAAUAGCAGGGUUUCCUGAGAAGGAGUUUGUUUUGCGACAAACGGACAAAGCAUAUG 6721	6782 GUGUGAAGGAUUGCGCGAUUACAAUGGUGUAGCCAGCGCUAUUUGCCAACUCACAAACA 6841 : :: ::	9 9 1	6962 TCAATATCAGGAACTCCAAGCAAATTAAAGTCGTCGGAGTGGAGGATAGGGATATTGCCA 7021 7022 UUCUUCAAAUGCCUAAAGACUUCCACCCUUUGCACAGAGGUAACGAUUAGAAAUCCAA 7081 7022 TTCTTCAAATGCCTAAAGACTTCCCACCCTTTGCACAGGGTTACGATTAGAAATCCAA 7081 7082 UAGUGGGUGAAUCAAUUUGUUGGUGGAAAUACGUUCCAAGAAAGUACAAUGCAA 7081		7202 UAGGAAGGAAGGAAGGAAUGGGGAUUGGCUUGGGGAUUGGGGAUUUGGGAUUUGGAAUUGGAAUUGGAUUGGAUUGGAAUUGGAAUUGGAAUUGGAAUUGGAAUUGGAAUUGGAAUUGGAAUUGGAAUUGGAAUUGGAAUUGGAAUUGAUGGAAUUGAAUGGAAUUGAAUGGCTTTAGCTTTAGTTAGTTAGTTAGTGATGGATTTATTG 7261 7262 UAGGAAUAGUUAAUAGGUUAAUAGGUAGAUCUAAGAAUAUGAUGAUUGGAAGUUGAAGGAAG
8 8 8 8 8	8 6 8 6	6686	8 6 6	8 6 8	\$ 8 \$	8 8 8 8	ପ ଓଡ଼ିଆ	6 6 6 6 6
Qy 5162 AUUACACAAAGACCAGCAUUCAUACGGGAAACGCAUACAAAGAUUGGGCAGGGUUGGUA 5221 Db ::		5462 ACCCUGAAAUUCACAGCAUUUAAUUCCUUACAAGUUAGAUGAAUCUGAAAUUCAACUUA 55 [GUAUAGGAAUCCAUCUUGAUUUACCGCGGAAGCAAAAAUUCCAUUCCAUUGUAGAAU	5642 TCCCAGATATGAAATACCGACACTTGTGGGAAGATATTCTCAAAATCAAGAGCATAAATT 5702 GUUUUGGUAGAAUGAGUGUUGUUACGCAACAAAAGUAGCAUAUACACUUAAAACAGACA [:::: :	5762 TTCATTCAATTGGAAAACTCTCGGATATATTGACGCCTCTTGCAAGAAGAATA 5822 AACAGCAUCAUUUJAAAGCAAUGACAAGAACGCAUGUAGUGGGAACACUUUUUC 5822 AACAGCATCATTTAAAGCAATGACAAGTAACGCATGTAGGGGAACACTTTTTC 5822 JAAGCAUAGCAAAUGCAAATGACAACAAUAUGCUAAGGACUACACAACAACAAUGCAA	5882 TAAGCATAGCAAATGCAAACGGAACCACTATGCTAAGGACTACACTGTGGCAATATTC 5942 AGAAAUGCAGGCAGCAAAGAAUCAAAAAAUCGGAAAUUCGUCAAUUAAAUUAAAUCGUU 5942 AGAAATGCAGGGAGCAAGAACAAATACTAAATTCGTGAATTGGTGAATTGATCCTTGATCCTTGATCCTTGATCCTTGATCCTTGATCCTTGATCCTTTAAATTCTTGAATTCGTCGAATTTAAATCTTGATCCTTT	Qy 6002 CGGCGAAAUGCGGAUUCCGAGGUUUGGAGCUUUAGAACUAGUUACCCAUCAGAGCAGGC 6061 Db 6002 CGGCGAAATGCGGATTCCAAGAGTTTCGGAGCTTTAGAACTTACCCATCAGAGCAGGC 6061 Qy 6062 AAGAAAUUUCAAAAUUUCUAAAAUUCGGAGUAAGGGAAAAGGCGAAAAGCACACACA	Qy 6122 AUAUCUVAGUVAGGUGGUCACUAUVGGUGGUUCUGGAUGAUAUGGGAUAAGUUCA 6181 Db - - - - - - - - - - - - - - - - - - -

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TGLPYHASRKGNVLLLERTREAGN HITTALEN ALGONTALENGOLLERGES TENNING SCRALNY FARNINGLES ALGONTALENGOLLERGES ALGONTALENGOLT ALGON
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WPTLLDVATGYFLKVFYPDVANAELENHUVDHYKKIIHVDSYSGLSTGYHILKTVTV
VEQLIKFTRONLESSLEHYRYGGTKWEDAHGASNIDNPQWGTRRLIKGYYRPKQLKED
MLTNPFLPLYALLSPGVILAFYNGGSLEYLMNYYIKADSNTAVLLVUKSLAKKVSAS
GYSTAQLQYYTERSLEPRANNYTSPSAANIVYGGACNRFLGANIHMSEPNNELASGGYT
ILEDHSITILEKSYLOLIDBANSELSWERGAIKYSSKQAIFSQENDLWQGSVDLGG
RYSESVISSYEWSRQRMKKLYSGLCNKTRNSVSWMSGKVSSSVCRTINYLVPDVFFFI
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SDVAEAYI EKRNQDRPYMPRYGLQRNLTDMSLARYAFDFYEMTSRTPI RAREAHIQMK
AAALRGANNNLFGLDGNVGTTVENTERHTTEDVNRINGINLLGVKGL"
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VIRGEHEGKLYDARIKVTRTMSHKIVHFSAAGANFWKGFDRCFLAYRGSDREHTCYTG
LDVTECGEVAALMCLAIFPCGKITCPDCITDSELSQGQASASSIRHRLVQLREVIKSS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    YPRFKHAVOILDRYEQSLHGENANYQDFAEIQSLTÖGMEKAAPPHANKLNAILIKGAT
ATGEBYEQAFKHLLEITRYMGNYTENIENGSRANKISGKAHINPTLMCDNQLDKN
ATGEBRYGAFKHLEFFSNYEEIIDPKKGYTOYETRIVPNGSRKLAIGKLIVYNFEVL
REQMRGERVYHAKREPSNYEEIIDPKKGYTOYETRIVPNGSRKLAIGKLIVYNFEVL
REQMRGEPVESHPITVECVSKSQGDFVHACCCVTTESGDPVLSDIKMPTKHHLVIGNS
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PEPPYATISANAPHLSEHIEERAKVHQAKROSEQELERIVAPAVALUĀMFDĀRRSD
POTKTINKLKGIVSTVPEPTVTHQALNDIEDDLTERNIEPDPĒLSSDSEIVQQLEĀBKT
FASWWSHQLSRGFTIPHYRTEGKFMTFTRATĀTĒVĀGRIAHESDKDILLMGAVGSGKS
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LHTETHEWWYHWKYNTSGISWGSLAID QAAQPAGLFKVSKLISDLDSTRYVAQTQONR
UMFEQLITGNIKAI JAFPESQLYFHYKGKCOMFDLXIKLHDBARBYFOPMLGOYQKSK
LINREAYAKDLLKYATPIEAGNI DCDLFBETVEI VI SDLWNYGFEVCNYVTBI DI FEA
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KVEANKTRTFTAAPLDTLLGGKVCVDDFNNQFYDHNLKAPWSVGMTKFYCGWDRLLQS
LPDGWIYCDADGSQFDSSLSPYLINAVLNIRLEFMEEWDIGGVMLRNLYTEIVYTPIS
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PERIVSILEWDRSKEPCHRLEAICAAMIESWGYDRLTHEIRKFYAWVIEQAPFNSLAQ
                                                                                                                                                                                                                                                                                                                                                                                                                       PVTOPKLHTWOFGSLDPIVVKGEAGSSVKETTRQLNVKEDVNLRCTATLEVVKPOSSI
VVRMQEEANRERAIFLDFENSLGRRPYGTAKNEKVIMTARGVSKIVPISTRKAMKHKRA
RERRRLEQPITLKWEPKLSEFSIGGGPSAKTIEEEETHTKWPLHKTPSTKKRTVHKKC
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                                                                                                                                                                                                                                                                                                                                                                                            translation="MAAVIFASAITNATINKLTSTGMVQFGSFPPVPLRSTTAITVVT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          KMDYQGI EMLMRSLIKI FKAKNANI EFTDKKTIKVDFVRKERTKFARIQVAHLLGKRC
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                                                                mosaic virus"
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/gene="HC-Pro"
/product="HC-Pro protein"
                                                                                                                                                                                                                                                           /codon_start=1
/product="polyprotein"
/protein_id="BAC79396.1"
/db_xref="G1:33146225"
                                                         organism="Turnip mosai
mol type="genomic RNA"
isolate="A64"
                                                                                                                                                        db_xref="taxon:12230"
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/product="P1 protein"
1181. .2554
ocation/Qualifiers
                                                                                                                                                                                              <1. .94
95. .9589
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                                 source
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CDS
FEATURES
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                                                                                               9601
                                                                                                                                                                                                                                                                                                9721
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Submitted (11-OCT-2002) Kazusato Ohshima, Saga University, Faculty
of Apriculture, Laboratory of Plant Virology; 1 Honjo-machi, Saga,
Saga 840-8502, Japan (E-mail:ohshimak@cc.saga-u.ac.jp,
Tel:81-952-28-8730, Fax:81-952-28-8709)
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Turnip mosaic virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
                                                                9662 GAAATTATGAGAAGCCATATATGCCGAGGTACGGTATTCAACGGAACCTCACCGACATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                9782 GGGAAGCCCACATCCAGATGAAAGCTGCAGCATTGCGAGATGCGAATAATAAGATGTTTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9662 GAAAUUAUGAGAAGCCAUAUAUGCCGAGGUACGGUAUUCAACGGAACCUCACCGACAUGA
                                                                                                                                                                                                                                                                                                                                                                                                                           9722 GUUUGGCGCGAUAUGCUUUUGAUUUCUAUGAAAUGACAUCAAGGACGCCCAGCUCGGGCCC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        9782 GGGAAGCCCACAUCCAGAUGAAAGCUGCAGCAUGCGAGAUGCGAAUAAUAAGAUGUUUG
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                                                                                                                                                            CCACUTUGCGUCAGAUTAUGGCUCACUTUAGCAAUGUUGCUGAAGCAUACAUCGAAAAGA
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Purnip mosaic virus gene for polyprotein, complete cds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mol. Ecol. 12 (8), 2099-2111 (2003)
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10142 TAAGCAAGGAGGG 10154
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AB093599
LOCUS
DEFINITION
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KEYWORDS
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Db 1202 TGGAAAGGATTGACAGATGCTTTCTTGCGTACCGTGGCAGTGATCGAGAGCACACG 1258	Qy 1657 UGCAAGGCCACUAUAAACGUUGAGGAGUGUGGCGAAAUGGCAGCCAUUGUAAACCAACUC 1716	Qy 1717 CUAUUUCCAAUGUGGAAAAUAACAUGCACUCAAUGUGGAGAACUGAAAUGAUGUCA 1776 1319 ATATTTCCTTGTGGCAAATAACTTGTCCGGACTGCATTACCGACAGTGAATTATCACAA 1378	OY 1777 CAAGAAGAACUUGAAUCUUUCAGGGGGGAAAAGGGGGCAAUUGGGAAGUAAAUUUCC 1836 Db 1379 GGCCAAGCAAGTGCATCCAGTATAAGGCACAGATTAGTTCAATTGAGGGAGG	QY 1837 AGUCUUCAUAUCAAAUUUCCUUACGAUCAUUUCUUAAUCGAUAUGAGAAUAGUCUG 1896 Db 1439 TCGAGCTATCCACGATTCAAACATGCAGTACAGATATAGATAG	OY 1897 AAUCGGAUGAACACAAACUUCGAUGCGCACAAACAAAUUGCACAAAUUGGCAGUCGC 1956 Db 1499 CACGGTGAAAACGCGAACTATCAGGATTTTGCAGAGATCCAAAGCCTGACGATGGAATG 1558	Oy 1957 AAAGAGAUUCCUUUUUCAAAUUUAGAGCAUCUGAAUUGAAUUGCUAAUUAAGUUGGGAUAAA 2016	2017 CUUGUUAGCGAGGAUUUCUAUGAAAUGUCUCAAUGCCUUUUAGAGCUAACACGCUGGCAU	Db 1619 GCAACAGGTGAAGAGTATGAACAACGAAGAACATTGCTAGAAATCACCCGGTACATG 1678 Qy 2077 AAAAACAGGAGGAGAUCAUUCAAGAAGGAAGAAGAUCACCAUUUCCGAAAUAAGAUGUCA 2136	Db 1679 AAGAATGCACTGAGAATATTGAGAAGGGATCACTAAAATTTTAGAATAAGATATCT 1738	OY 2137 GGUAAAGCACAAUUUAAUUUUGCAUUGAUGUGUGACAACCAAC	Oy 2197 UUCGUGUGGGGUGAAAGAGGUVAUCAUGCGAAGAGGUUUUUUUUUU	2257	2317 CAPACAGCUAUAGGAAAACUGAUUUUAUCGACGGAUCCAUCUACGCUACGACAACAAUG	Db 1919 AAACTTGCTATTGGCAAGCTCATAGTTCCAACAAACTTCGAGGTCTTGAGGGAGCAAATG 1978 Qy 2377 AAAGGUAGCCCAAUCACAAGAGUUCCCAGUUGGUAAAUAUUGUACAAGCAAAAGAGAUGGU 2436 Dh.	2437 UGUUACGUCUAUCCAGCAUGCUGUUACAAUGGAAGAUGGUACGCCAUUGUUUUCUGAU	DD	2557 GAUGUACCAAGCAGCUCAAGUGACAUGAUGUGGCUAAGGAAGGUUAUUGUUAUCUC 	OY 2614 AACAUUUUCUUGGCAAUGUUGCUGAAUGAGAAUGAAGGAAUCAAAAUCAAAAUCACAAAG 2673 Db 2219 AACATATTTCTCGCAATGCTAGTGAATGTCAAAGGAATCACAAGGAATCACAAGGAATTCACCAAG 2278	2674
mat_peptide 25553619	rotein"	/product="6K1 protein" 3776. :5707 /gene="CI" /product="CI protein"		/gene="NIa-VPg" /product="NIa-VPg protein" mat_peptide 64437171 /gene="NIa-Pro"	/product="NIa-Pro protein" 71728722 /gene="NIb" /product="NIb protein"	.tein"	/gene="P1" 11812554 /gene="HC-Pro"				/gene="NIa-VPg" 64437171 /gene="NIa-Pro" 71728722	/gene="NIb" 87239586 /gene="CP" ofen oras	23.5%; Score 2385; DB 14; Length 9798;	Similarity 41.2%; Pred. No. 0; 6; Conservative 1286; Mismatches 3730; Indels 109; Gaps 14; CACUUGGAGAACUUAGAAAAAAAAAAAAAAAAAAAAAAA	961 1416	1021 1476	1081 1536	1141 1596	TGTGĆATTTJAĠTGCGĠĊŔĠŦGGTAACTTC 1201 CAUUCGAGAUAGACCUAAGAACGCUCAUGAG 1656

9142 8786 8302 7970 8362 8030 8422 8090 8482 8150 8542 8210 8602 8270 8722 8782 ||||| || || ::|| |GRAAAAGCCCCTTACATAGCAGAAACAGCACTCAGAAAGCTTTACCTTG 8630 9082 8726 AAAAAUAAAGAAGUCGAGAAGAACAUGAGAAAACUUCGAAUAGCGCAU 9202 8182 7850 UUAGAAGCGAUUUGCGCUUCGAUGAUUGAAGCAUGGGGUUACCCUAGGU 8842 Auriceana auruna uge un gegune un gang canaca aucane 8902 |: || || ::::|:|| :|||: |||| : ||||||| |||: ||| BATACGCAAGTTTTATGCGTGGGTGATTGAACAAGCTCCATTCAACTCCT 8570 AGUGCUGAUGAAAUCAUGUCAUACUUAGAGAUGUGUGCAAGUGAUUUGA 9022 JGUUUCAAACAACGAAAAAGACAAGGAUGUCGAUGUAGGAUCAAGUGGAU 9262 idatectegtttgacagaaggaaggaaaggaaaggaaagg UUUUDUGAUCUUAAUAUGAAAUGCCCAUGGACAGUCGGGAUGACUAAGU ceaumeacaeuncucumacaccauacuocueaauecaeuacuceeea TUACACCCCCAUUGCAACACCCUGAUGGAACAGUCGUCAAAAAGUTUCGAG IGGUCAACCGUCAACAGUCGUAGAUAACACAUUGAUGGUCUGUAUUUGUG IUUAAUUAUGAAUAGUGUAAAGUUUGAGAAUCAGGAUGAUGUCUGCAGGU GAGCCAGAGAGGGUUGUCUCAAUACUUGAGUGGGAUAGAAGUGUAAAAC suacunucau de auca a concurca con concurca de concurca GAAAACAAGAAGACGAUGAAGAGAGAAAGAAUAAAGAAGAAAAGCAGG NUCAUGGAAGAUUGGGACAUAGGCGUGCAGAUGCUUCGAAAUUUGCACA

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Japanese yam mosaic virus
Japanese yam mosaic virus
Japanese yam mosaic virus
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                                                   CUUTICAUCAUACCACGAAUUAAAUCGAUAUCCAAUAAACUCACAAUGCCAAAAGUGAAAG
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Complete nucleotide sequence of the genomic RNA of a mild a dapanese yam mosaic potyvirus
Arch. Virol. 145 (3), 635-640 (2000)
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Japanese yam mosaic virus genomic RNA, complete genome.
ABO27007
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Direct Submission
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/tränslation="MATCVGKLAETSLNNTIAPQLQPGTLPPVFIGIPATSCKTIATD
KNDEHVIQSKSTEAQKKANVNNKAFIHKAHAEYNKQCAVLDKWEEEYNTTRSTNPSSY
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AELKWPLHQTRSQRIKGTPKQPVTLGRGEFAKFVKNLTTLMTQKSLLLELCGKHVHRV
CVRREHKKVYLKINTKHEEGFNKARDVVMDNPTQRLLELMITRTSGNNRHSVQNIKPG
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WNGFNTAFQRYRKQDREHTCETDLDVEECGEVAALLCLALFPCGKITCNKCVEENLLS
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EGKTL PAFSQANRI NDVL I KGGSATAEELSEATRNLLEI VRYLKNRTESSEKGTLKTF
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INPRGQKRYATTRLI VPTNFEVLREDQNGGES IGEHPLIVECSYSJLADBELFPCCCYTN
EAGEP I LSELQMPFTKAHLVVGNSGDSKYVDNPPQEGGSWYI AKAGFCYMNI FLAMLVN
VRKEEAKAFTKMVRDVLI NQLGTWPTLLDVASACYLLKVFFPDVSSAELPRI MVDHKT
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ODLSELGFFTPCQYITDBDYIFNALINKSAYGALKYGYKEKYPEYBOFTGRKKTILLKQSC
ARLYGKMGLMNGSLKABLRPLEKVQANKTRFFTAAPLDTLLGGKACVDFNNGFYEL
NIKGPWSVGMTKFYGGWNELLIKLPDGWIHCDADGSQFDSSLSPYLINAVLNIRLHFM
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SKQQTVINLEKDVNVGTVGTFAVPRLKGLATKMSMPRVRGKAAMNLDHLLVYNPEQVD
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Submitted (07-MAY-1999) Shin-ichi Fuji, Akita Prefectural University, Faculty of Bioresource Science; Shimoshinjo, Akita, Akita 010-0146, Shaman (E-mail:sfuji@akita-pu.ac.jp, Tel:81-18-872-1640, Pax:81.18-872-1678)
                                                                                                                                                                  mosaic virus"
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/protein_id="BAA86288.1"
/db_xref="GI:6277343"
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1. .9760
/organism="Japanese yam
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DB 14; Length 9760;

Best Local S Matches 3517	al Similarity 40.7%; Pred. No. 0; 3517; Conservative 1340; Mismatches 3668; Indels 121; Gaps 17;	名 &	2500 AAGAUGCCAACUAA
-	1420 GGGCACACUGGACAUAUCAUGAUAUGAUAAGUUJAGAGGUUUGAGUGGACGGCAUUUC 1479 1420 GGCACATAGTGGTTTGTCTTGAATAGAGACTTTATGGCACACAATCTGGTGCATAT 1038	୍ ପ	: 2056 CAAATGCCAACAA
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W	2200 GUGUGGGGUGAAAGAGGUUAUCAUGCGAAGAGUUUUUCUUAAACUUCUUUGAGAAGUU 2259	' සි	: :: 2836 CAGTATATCATTG
-	GTTTGGGGTGAAAGAGGATATCATGCCAAACGGTTCTTTAATAAATA	ò	3310 GCGCUUCUUCAACT
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-	GATCCTAGCAAAGGATATGCAAAATTTGAAGCACGTATAAACCCAAGGGGCCAACGCAAA	õ	3370 GCGGAUUCAGCAL
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4741 4324 4801 4384 4861 4444 4921 4981 4564 5041 4624 5101 4684 5161 4744 5221 5281 4864 5341 4924 5401 5461 5044 5521 5104 5581 5164 5641 5224 5701 5702 GUUUUGGUAGAAUGAGUGUUGUUAGCGCAACAAAAGUAGCAUAUACACUUAAAACAGACA 5761 4625 GAAAACATTTTGTCGTGGCAACGAACATCATCGAGAATGGAATTGGAGTCACATTGGATATTGAAG UUGCAAAUAAUCCUCUAAAAUUAAGUGAUTUUGAAUTUUGUGAUAAUAGAUGAGUGUCACG CUGGGUCUGCACGAGAUGUAAUCAAUAAGGGAGACAACAUUUUAGUGUAUGUUGCUAGUU 4922 ACAAUGAGGUUGAUCAGCUCUCAAAAAUGCUCGGAGAUAAAGGCUAUUUAGUGACUAAAG UCGAUGGGCGUACCAUGAAAAUUGGUUCGACCGACAUAGUUACUAAAGGGAGUAGCCAGA 5042 AGAAACAUTUCAUTGUAGCAACCAACAUAAUCGAGAAUGGAGUCACUCUAGAUGUAGAUG UNGUUGUGGACUTUGGUUUGAAAGUCACUGCUGAAAUUGAUUACGACAACCGGUGCGUUA CUAGUCUUGUGGCGACACACGCCUGCAUUCCAAUGCUUCACAUAUGGAUUGCCUGUAAUGA 5342 CACAAGGAGUUUCAGUUAACAGUUUAUCAAAUUGCACAGUCCGACAGGCCAGAGUUAUGU 5462 ACCCUGAAAUUCACAAGCAUUUAAUUCCUUACAAGUUAGAAUGUGAAAUUCAACUUA 5522 GUGCCAUGGCUUUUAACUUUACCGUAACAUCUAUTUGGCUAGAUUGUAAAUUTUAUGACA 5582 GUAUAGGAAUCCAUCUUGAUUUACCGCGCGAAGCAAAAUUCCAUUCCAUUGUAGAAU 5642 UCCCAGAUAUGAAAUACCGACACTUGUGGGAAGAUAUUCUCAAAAUCAAGAGCAUAAAUU UCCUAGAUAGCAACGCUAUGGCAUUCGUGUCUUCUCAAAGAACAACUAUGAUGGCA CAGUIUCCAUUCAUAUAGAGGAACAACUUAGUIUUCCAAGCUUUUUGUGAAGCUCAAGGAA cuceunungagungccgccunacunnanggcuncacungnanacanganggcagcangc 4622 4682 4742 4802 4862 4445 4982 5102 5282 5402

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PN JP 20013002.

PN JP 20013002.

PD 31-CCT-2000

PF 21-APR-1999 JP 1999113671

PR SHINITH FUJI, HITOSHI NAKAMAE, TOSHIHIRO KATO, TAKAMAC.

PLISASHI IWATA

PC C12N15/09, A01H5/00, C12N15/00, C12N15/00, C12R1:92), PC (C12N7/04, C12R1:92), C12N15/00, C12N15
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                                                                                                                                                                                                                                                                                                                                                                   Potyviridae;
                                     Attenuated strain of Dioscorea japonica mosaic virus, Dioscorea japonica mosaic virus, Dioscorea japonica mosaic virus free strant crop and cultivation method japonica mosaic virus.
                                                                                                                                                                                                                                                                                                                                                                                                                     1 (bases 1 to 9760)
Fuji,S., Nakamae,H., Kato,T., Ida,T. and Iwata,H.
Attenuated strain of Dioscorea japonica mosaic virus, Dioscorea japonica mosaic virus resistant crop and cultivation method thereof, nucleic acid, and diagnosis method of gene of Dioscorea
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                                                                                                                                                                                                                                                                                                                                                                   stage;
                                                                                                                                                                                                                                                                                                                                                                   no DNA

    .9760
    /organism="Japanese yam mosaic virus"
/Mol_type="genomic RNA"
    /db_xref="taxon:79917"

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JP 2000300270-A/1.
Japanese yam mosaic virus
Japanese yam mosaic virus
Viruses; ssRNA positive-strand viruses, 1
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AICHI PREF
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                                                           LOCUS
DEFINITION
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KEYWORDS
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Ob 7922 ACATAAGATTACATTTCATGGAAACAT	8360	8420	8480	Qy 8540 GGUAUUUCGUUAACGGGGAUGAUUUAU 	8600	Qy 8660 CGAAAACAAAGAGAACUUUGGUUUA 	Oy 8720 AUAUUCCAAAGCUGAGCCAGAGAGGG 	8780		Oy 8900 AUCUCGCAUCUGAGGGAAGGACCAU 	8582	9017		9137 8762	Qy 9197 GCGCAUCUGGUGCUAUUGAUGAACAA 	9257		Oy 9377 ACAUUCAAAUACCAGGCAAGUAUUU
: : :: :: : : : :	7280 UGAGUCAUAAGUACGAUCAUAAUUAUUCUCGAACUUUGACGACGCGUUUGAAGGCGAUU 7339 	7340 AUAUUAACAAGUUGAAGCAACCAGAAGUGGGACCAGAAUUGGACUUACAACGUUAAUACUG 7399 	7400 UUAGUUGGGGAACAUGAAACUUCAGGAUAGUGCUCCAUGCAAAGAAUUCAAAACAACUA 7459 	7460 AGUUGAUUAGCGACUGACGGAAACCUGUGGGGCUCAGAGUAGCAAUCAAGUUAGAU 7519 :: ::	GGUDADADAACGAAAAUUUGAAGGGGUUGCAACUAUUCCGAAUAACUUUG : :	7580 UUACAAAGCACUUGUGAAAGGACGAUGUAAAUUGUUUGAAUUGUAUCGAACUGCAAACUCGUA 7639 :: : : : :	7699	7759	7760 ACACUGAGAGAUUUGAAGAUGCAGUUGGGCAAGUCAUCGAAAUUAUGAUGCAAUGGAACU 7819	7820 UUAGGGAAUGCAAGUAUGACCCGAUUGGAUCUUGAAUCAUUGAACAUGAAAG 1879 :- - - - - - - - - - - - - -	UUGUACAGUGGUAGAAAAUUCCACAUUUG 7939 ::	7999 7621	8000 UUUGGAAUGGAAGUCUVAAAGCUGAAUVAAGACCAAUGAAAAGGUUGAAGCAACAAAA 8059 : :	8060 GGCGAACAUUCACAGCUCCAAUUGAAACUUUACUUGGGGGAAAGGUUUGGGUCGAUG 8119	8179	AGUUUNAUVGCGGANGGAAUGAUCUVCUAGGUAAACUUCCUGAUGGUUGGAUAUACCGCG 8239 :::: : : :::	8240 AUGCUGACGGAUCACGAUUUGACAGUUCUUACACCAUACUUGCUGAAUGCAGUGCUCG 8299 	8300 GGAUUAGGGAGUUUUUCAUGGAAGUUGGGAAUGGGGGGGG
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8539 GUUGUCUCAAUACUUGAGUGGAUAGAAGUGUAA 8779 |--||-||-|||-|| |-|| |-|| |ATIGTCTCAATACTIGAATGGGATCAAAGG 8401 UUGCUUGCAAUCAAUCCAAAAUUUAUACACAUCC 8599 8221 AAAGACGAUGAAGAGAAAGAAUAAAGAAGAAA 9136 8761 9316 || |:||: || |||||| : |:||: : : : ACTGTGGACACACACTTATGGGTGTTATTAG 8101 AAUTUVAGGUTUVAGACUVACGAUTUCUCUCAUCGAA 8659 UGCGCUUCGAUGAUUGAAGCAUGGGGUUACCCUA 8839 :|||||: | |:||: ||| ||:||||: ||| TGCGCTGCAATGATAGAATCATGGGGTCACCAAG 8461 UAUGCUUGGGUUCUGGAACAAGCACCAUACAAUC 8899 AUCAUGUCAUACUU---AGAGAUGUGUGCAAGUG 9016 SAUGAAGAUGUUUCUCAÇCAGUCCGCUCUUGAUG 9076 | | | : ||:|| STATATCATCAAAGTGGCGACGACACGTTGGATG 8701 SAAGUCGAGAAGAACAUGAGAAACUUCGAAUA 9196 CCGCCGATGACCCAACGGCAAAGCAAGCAAC 8821 9376 TGGGACATAGGGGAGCAAATGCTGCGGAATTTAT 7981 ACAGUCGUAGAUAACACAUUGAUGGUCUGUAUUU 8479 UACAUTUCGGAAACAGCGCUCAAAAGACUUTUACA 8959 AAAGGACTTGCAACAAAAATGAGCATGCCTAGAG 8923 :| :: | : | | | | | : | CTGATTAGTATAGACCCTTC AGGAAGCAAGAAGCCCAACCCACTCAAGGCA AGUGUAAAGUUUGAGAAUCAGGAUGAUGUCUGCA |: | | : : : | | : : : | | | ATTGAGGTTTAATGTAGAGCAATATTTGAAGATT AAAUCGAUAUCCAAUAAACUCACAAUGCCAAAAG SAGUUCCUUUUACAAAACACACAGAUCAAGUGG GCAACACCUGAUGGAACAGUCGUCAAAAAGUUUC

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SEBLISELÇMQPTKNHLVVGNSGOBKYVDNPPQQQSQXITARAGYYCYNDI TELAMINUNR
KEBARAFTKMYRDVILINQLGTWPSILLDVASACYLLKVFPDVSGAELPR IMVDHKTVT
MHVIDSYGSLNTGYHILKANITVEQLIKFTRAGLKSDWKHYLIGGPVLNNEDIDPIEYR
TESPHLKKLIKLIKGIYNDPQLILDDIRIDRYLDFLALLSFQVLIAMYNSASELBILTRERYMR
KUDBEVAIVLILESLARKVSVGTSLLSQLILIEGEAQVIIBAVOGIRQRYPIPYTVVM
EMLIILASRSSBDAALDAAGPKKFQRESVQLMEKNYLRILEDEWRGLSWRQKFSAILR
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RTGKALQVDULTPHPPLLVCANRPTIAGFPERRYELRGYGGPRAISLKDVPKSNDLSE
MVQHESALLHRGLRDYNPISNICKLINRSGERDTWYGIGFGPV1ITNRHLFBHVG
BLDIKTRHGDFLIANTTKLOLYPVPNRDLILIRLPKDIPPFQKLQFRQPERNEKICM
VGSNPQAKSYTNTVSEFSILLDMDDCHFWHMH TYTKOQCGELEJVSTRYNIYGHSLGL
GSLNYTINYPASFPERFVSGYLLTPENHQWIQHWKNYTDNISGGELEJVSTRYGNIYGHTSL
TTKLIGDLESLFVRQWKREKWYTQLDGNLKAIASCPNQLYTKHVVKGKCPMFDMYL
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LEELGFETOOYITDEDVIFNALIMKGANGALYGOKKRERYFRDFTOEMHQILKOSCAR
LYTGKWGLMNGSLKAELRPLEKOVANKTTFTAAPLDTLGGKTCVDDFNNOPFELNI
KGPWSVGMTKFYGGMSELLFKLPDKWVHCDADGSQFDSSLSPYLINAVLNIRLHFWES
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YAFDFYEVTSKTPARAREAHIQMKAAALRGVQNKLFGLDGNVSTMEENTERHTAEDVN
RNMHSLLGVRGV"
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QATHENILRKOOEIRQIVFORHPOFKHALQILERQSKALOSVNSNYKDFTEIHSLSEG
KTLSAFSHASRINDVLIKGGSATAEELSEATRNLLEIVRYLKORMESSEKGTLKTFRN
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CRRHKK1YLKVHTMHEKGFNRARDVK1ENFAQH1LELMVARTSGNNWHSVRD1KPGYS
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                                                                                                                                                                                                   'translation="MAICIEKLTNPNLSDSPVFQLQFGTLPPVTISVTDSTNVTAMET"
                                                                                                                                                                                                                                     DLKPGKONKPTDAORKVNDNKAFIOSMHSEYTKOCTTLDKWEEEYNKARSMRPNSYKL
                                                                                                                                                                                                                                                                    VQTRQQRKAMLKRSMEKTSKQLKEQTDILEKCVIGPWGPPMNTFSIAAGPLPSAMETE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SSKFAIHTRGGLHNKSIEDLGGRYGESMSSYFGELKNGAANACKKLTTQAKTITQSTF
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Best Local Similarity 40.6%; Pred. No. 0;
Matches 3480; Conservative 1312; Mismatches 3668; Indels 111; Gaps
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'protein_id="BAA36278.1"
'db_xref="G1:4092844"
xref="taxon:79917"
                                     CDS
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Japanese yam mosaic virus gene for polyprotein, complete cds.
AB016500
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Japanese yam mosaic virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
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                                                                                                                                                                                                      9164 AGCAAATTGAATATCCGATAAAACCATTAATAGATCACGCCAAACCCCACATTTGACAA
                                                                                                                                                                                                                                                                                                                                                                                                                                        9617 UUAUGGCUCACUUUAGCAAUGUUGCUGAAGCAUACAUCGAAAAGAGAAAUUAUGAGAAGC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9404 AAATGAAAGCAGCAGCAGCCTTAGAGGTGTGCAAAACAAGTTGTTTGGATTGGACGGAAATG
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                                     AAUCCUAUGGUGUGUCUGAUGAAGAAAUGGGAAUAAUUUUGAAUGGAUUAAUGGUUUGGU
                                                                                               9044 GAGATTACCAGTTGGATGACAGCTCAATGCAATAATCCTGAATGGATTGATGGTTTGCT
                                                                                                                                                                       GUAUUGAAAAUGGAACAUCUCCAAACAUUAAUGGCAUGUGGUUUAUGAUGAUGCAAGGGGAAG
                                                                                                                                                                                                                                                                                                      AACAAAUCGAAUACCCCCUUCAACCAAUAGUGGAAAACGCAAAACCCACUUUGCGUCAGA
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/mol_type="genomic RNA"
/strain="Japanese yam 1"
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Arch. Virol. 144 (2), 231-240 (1999)
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Fuji, S. and Nakamae, H.
Direct Submission
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5293 4394 TGACGGAAGAAACATTGGGTTTAAAGCAGTTTGTGGATGCTCAAGGCACTGGTGCAACT ACATAATATCGAAGGCATTGATTGATAAGGGATACAAAGTCACAAAAGTCGATGGGAGAA TCGGGACGAAGGTTGTACCCTTTTTGGATGTTGACAATAGAATGATGCAATATCAAAAG CCAGCAUTUCAUACGGAGAACGCAUACAAAGAUUGGGCAGGGUUGGUAGACACAAGAAAG CGACACAGGCUGCAUTUCAAUGCUUCACAUAUGGAUUGCCUGUAAUGACACAAGGAGUUU CAGUUAACAGUUUAUCAAAUUGCACAGUCCGACAGGCCCAGAGUUAUGUCUCGUUUUGAGU ACAAGCAUUUAAUUCCUUACAAGUUAGAUGAAUCUGAAAUUCAACUUAGUGCCAUGGCUU UUAACUUUACCGUAACAUCUAUUUGGCUAGAUUGUAAAUUUUAUGACAGUAUAGGAAAUCC AUCUUGAUUUACCGCGCGAAGCAAAAUUCCAUUCCAUUGUAGAGAAUUCCCAGAUAUGA 5654 AAUACCGACACUUGUGGGAAGAUAUUCUCAAAAUCAAGAGCAUAAAUUGUUUGGUAGAA GAAAAACUCUCGGAUAUAUUGACGCCCUCUUGCAAGAAGAAUAUAGAAAACAGCAUCAUU UNAAAGCAAUGACAAGUAACGCAUGUAGUGGGAACACUUUUUCAAUGCUAAGCAUAGCAA GAGAUGUAAUCAAUAAGGGAGACAACAUUUUAGUGUAUGUUGCUAGUUACAAUGAGGUUG AUCAGCUCUCAAAAAUGCUCGGAGAUAAAGGCUAUUUAGUGACUAAAAGUCGAUGGGCGUA CCAUGAAAAUUGGUUCGACCGACAUAGUUACUAAAGGGAGUAGCCAGAAGAACAUUUCA UUGUAGCAACCAACAUAAUCGAGAAUGGAGUCACUCUAGAUGUAGAUGUUGUGGGACU rcscaarcaartargaagagagaartrcagagarraggacgrgrrggacgacaaarcag UGCCGCCUUACUUUAUGGCUUCACUUGUAUAUCAUGAUGGCAGCAUGCACCCUGAAAUUC

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7171 6853 6913 6973 7411 7471 7150 ::|||||| : : || :|| || | | : || || 331 TTAAGGACATTATGAAGTACTACAATGATGATCAACCTCACAAT 7390 7450 7570 7111 6733 6734 CAAACTTCCAGGCAAAGAGCGTAACAAATACAGTATCGGAAACAAGCATTATATTTACCAA 6793 7231 7093 7531 7711 7712 UNAAGGACCUAUUNAAAUACUCAUCAGAAAUACCAAUUGGGGGGGUCGACACUGAGAGAU 7771 7891 | :| |: || ||: || ||: ||: ||: ||: || ||: ||: ||||| ||||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: ||: | 7951 CUTUDAGUUAGUCACUGAUGGAUTUAUUGUAGGAAUACAUAGUUUAAUGAGUCAUAAGU 7291 7292 ACGAUCAUAAUUAUTUCUCGAACUTUGACGGGGGGGTUUGAAGGCGAUUAUAUAUAAGAGU 7351 7592 UUGUGAAAGGACGAUGUAAAUUGUUUGAAUUGUAUCUGCAAACUCGUAGUGAAGCGAAUG 7651 7772 UUGAAGAUGCAGUUGGGCAAGUCAUCGAAAUUAUGAUGCAAUGGAACUUUAGGGAAUGCA 7831 :: |||| | :: ||: ||| ||| ||| 6674 TTCCACAAAAAAATTTGTATGGTAGGCT 6794 TGGATGACTGTCACTTTTGGAAACACTGGATCACCACAAAAGACGGTCAATGTGGATTGC 6854 CCTIGGTIAGCACGAGAGTCGGCAACAIAGTCGGCAITCAIAGTCTCGGAAGTCTCAACA CGUUGUACAGUGGUAAGAAAAAAGGCGUACUUCGAAAAUUCCACAUUUGAUGAUCGAAAAUC 7172 GAGUUGAAGGUAGUUUUUGGAAACAUUGGAUUAAUACAACGGAAGGACAUUGUGAUUGC 7352 UGAAGGAACUGAAAUGGGAGCAGAAUUGGACUUACAACGUUAAUACUGUUAGUUGGGGCA 7412 ACAUGAACUUCAGGAUAGUGCUCCAUGCAAAGAAUUCAAAACAACUAAGUUGAUUAGCG 7472 ACTUAUGCACGGAACCUGUGUGCGCCUCAGAGUAGCAAUCAAGUUAGAUGGUUAUAUAAUC AGUUCUUUAAACCACUGAUGGGUUUCUAUGGGAAGAGCGGUCUCAACAAGGAAGCAUACA 7232 7652

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ILROYASITILEKSYYLOLIUDARANIVENSGYSKQAIRSGYGYDLPWQSGYDLGG
RYSESVISSYEWSRQRMKRLYSGMCNKTRNSVSWVSSKISGSVCRTINYLVPDVPRFI
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FGEAYTKKGKSKGRTRGLGHKNRKFINMYGFDPEDFSAVRFWDFLTGATLDENPFTDI
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GNFIWGERGYHAKRPFSNYFEIIDPKKGYTQYETRIVPNGSRKLAIGKLIVPTNFEVL
REQMRGEPVEPHPITVECVSKSQGDFVHACCCVTTESGDPVLSDIKMPTKHHLVIGNS
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FDEFVAYINEKAPHLSEYI EFEEKAVTHQAKROSEQELERI IAPIALVLAMFDAERSD
CVTKI LNKLKGLVSTVEPTVYHQALNDI EDDILSERNLFVDFELSSDSEMI QQLPAERT
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TGLPYHLSRKGNVLLLEPTRPLAENVHKQLSOAPFYQWTTRMGCLTAFGSAP ISOWT
SGFALNY FANNRAR TEEFDFVI FDECHVHDAAMAMRCLLHEONSGKI IKVSATPPR
REVERSTQYPVTISTEDTLSPQDFVNAQGSGSNCDVISKGDNILVYVASYNEVDTLSK
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KVLPYLDTDRIMLSTIKTS I RYGER I QRLGRVGRHKPGHALR I GHTERKLISEVDESCI A
TERALK CFTYGLP VI TINNYST SI I LGAVTVKQARTMS VE EI T PFYTSQVVR YDGSMHPQ
VHALLKR FKLRDSE I ALINKLA I PNRGVNAWLPASEYAR IGANVEDRRDVR I FFMCRDI
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EGKAPYI AETALRKLYLDKEPSQEDLTQYLEAI FEDYEEGTEVCVYHQADETLDAGLT
EEQKQAEKERKEREKTEKEREKQKQLALKKGKGSAQEDGERDKEVNAGTSGTFSVPRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        VIRGEHEGKLYDARVKVTKAMSHKIVHPSAAGNNFWKGFDRCFLAYRSNDREHTCYTG
LDVTECGEVAALMCLAMFPCGKITCPDCVTDSELVQGQASTPNIRHRLAQLREVIKSS
YPRPKHAVQILDRYEQSLNGENANYQDFAEIQGLSDGMEKAAFPHANKLNAILIKGAT
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LHATIAGFPEREFELRQTGKARPINIDEVPKANTEVVPVDHESSSMFRGLRDYNPISN
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PVENSKFWKHWI STKDGQCGS PMVSTKDGKI LGLHSLANFQNSI NY PAAFPDDFAEKY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVAQPKLCTVQFGSLDPVVVKGGAGSSAKATRQQPNGEIDVSLREAAALEVAKSKPNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RERRNSQQQITLKWBPRLSEISIGGGPSASEIEVEEVRTKWPLHKTPSMKEKTVHKVP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RMNGOGIDMLMRSLIKI FKAKNANI EYTGRKSVRVDFIKKERVNFARVOVAHLLGKRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       QRDLLTGVEENRFIDMLSDYSGNKRTINPGVVRAGWSGIIVRNGALTQERSRSPSKAF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LHT PETHEWVKHWKYNTSGISWGSLNIQAAQPAGLFKVSKLISDLDSTAVYAQTQQNR
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                                                                                                                                                                                      Direct Submission
Submitted (11-0CT-2002) Kazusato Ohshima, Saga University, Faculty
Submitted (11-0CT-2002) Kazusato Ohshima, Saga University, Faculty
Saga 840-8502, Japan (E-mail:ohshima/@cc.saga-u.ac.jp,
Tel:81-952-28-8730, Fax:81-952-28-8709)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                              1. .9798
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Mol. Ecol. 12 (8), 2099-2111 (2003)
22745497
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                                                                                 12859632
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CDS
                                                                                                                                                      AUTHORS
TITLE
JOURNAL
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REFERENCE
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KSLASKORVPKYEKRLALNLDHLILYTPEQTDLSNTRSTQKQFNTWFEGVMADYELTE
SDVOQ1ILNEALMVWC1ENGTSSNINGWWWWMDGDOGYGEPLIKPLIDHAKETFRQIMAHF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1556 UGAUCAACAUGACCCACUACAGUGAUGCAGGUUUGAGGUUUUGGAAAGGUUUUGAUCGUC 1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1101 TCAGGGGTGAACATGAAGGCAAATTGTATGATGCCAGAGTAAAAGGTCACAAAAATGATGA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1616 AAUUUAUUGACAUUCGAGAUAGACCUAAGAACGCUCAUGAGUGCAAGGCCACUAUAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            23.0%; Score 2337.2; DB 14; Length 9798; llarity 41.0%; Pred. No. 0; Conservative 1260; Mismatches 3658; Indels 105;
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5867. .6442
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5708. .5866
                                                          95. .1180
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9590. .9798
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3776. .5707
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Matches 3487; Conserv
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S'UTR CDS

FEATURES

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RYSASVISSYEWSKOORKGYKSSIANKLRSSKWSWTSSKVSNYCKTINTIVPDVEREN
NULVCISLLIKWTREANOIVTTORRIKLDIEETERRIKIEWELAFHSKLTOSAGOHPT
LDEFTAYIAEKAPHLSEHIEDEEKAVVHORRIKEROSEGELERVIAFVALVLAMFDAERSD
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FASWWSHOLSRGFTIPHYTTERKERFWTFTRATATEVAGKIAHESDKDILLMGAVGSGKS
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SGFALNY FANNRSNIESTEDTLSFODETWANAMARCLLHECDYSGKIIKVSATPPG
REVERSTOYPYTISTEDTLSFODETWANGGSGSNCDVVSKGDNILVYVASYNBUDTLSK
LILIERDFKYTKVDGRTWKVGNIEITTSGTPSKKHFIVATNIIBKGYTLDIDVVADPGT
KVLPYLDTDNRMLSTTRTSINYGSRIQARLGKWGRKFPGHALRIGHTEKGLSEVPSCIA
TEAALKCFTYGLPVITNUSTSILGWYTVKQARTWSVFEVTPFYSOVVRYDGSWHPO
VHALLKRFKLRDSETVLNKLAIPNRGVNAMLTASEYARLGANVEDRRDVRIPFFMCRDI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             QRDLLAGVEENHFIDILSEYSCNKTVINPGVVCAGWSGVIVRNEVLTQKRSRSPSKAF
VIRGEHEGKLYDARIKITKTMSLKIVHFSAAGANFWKGFDRCFLAYRSDNREHTCYSG
LDVTECGEVAALMCLAMFPCGKITCPDCVTDSELSQGQASGPSMKHRLTQLRDVIKSS
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QSVLAQLQIIERSLPELVEARANINGPDGAASRACNRFWGMLLHWAEPNYELANGGYT
TLRDHSISILEKSYLQILDEAWNELSWSBRCVIRYYSSKQAIFTQKDLPMQSGADLGG
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VLGGGVWWVOVGHLRSKISBPTHEAKGKRQRQYLKFRRNARDNRWGREWYGDDDTIEHF
FGDAYTKGKGKSKGRTRGIGHQNRFYINMYGFDPEDFSAVRFVDFLTGATLDDNFFTDI
TLVQKHFGDIRMDLLGEDELDPNEIRVNKTIQAYYMNNKTGKALKVDLTPHIPLKVVD
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LLLSVHPEYEYILDTMADNFRELGLKYTFDSRTKEKGDLWFMSHQGHRREGIMIPKLE
PERIVSILEWDRSKEPCHRLEAICAAMIESWGYDKLTHEIRKFYAWMIEQAPFSSLAQ
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EGKQARKEKKGRERRAKEREREKQKQLALKKGKOVAQEEGKRYDKEVNAGISGGT FEVPRI.
KSLTSKARVPPRYEKRVALNI.DHI. I LYTPBQTDI.SNTRETRKQPTAPFEGYMADYELTE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     translation="MAAVTFASAITNAIINKPTSTEMVQFGSFPPMPLRSTTITTVAT"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PVAQPKLYTVQFGSLDPVVVKGGAGSLAKATRQQPNVEIDVSLSEAAALEVAKPKSSA
VLRMHEEANKERALFLDWETGLKRRSHGIAENEKVVMTTRGVSKIVPRSRAMKQERA
RERRRAQQPITLKWEPKLSEPSIGGGSSASAIEAEEVRTKWPLHKTPSLKKRNVHKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YPRFKHAVQI LDRYEQSLSSANENYQDPAEIQSI SDGVEKAAFPHVNKLNAI LIKGAT
ATGEEFSQATKHLLEI ARYLKNRTENI EKGSLKSFRNKVSQKAHINPTLMCDNQLDKN
GNFI WGERGYHAKRFPSNYFEVI DPKKGYTQY ETRI VPNGSRKLAIGKLI VPTNPEVL
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GDPKTIDLPBETEBNKMYTBAGSVCYTHSTLAMLVNKEPGAKEFTKVNKDKLVSELGK
WPSLLDVATACYFYKVFYPDVANAELPRMLVDHKTKIIHVVDSYGSLSTGYHVKTKUT
VEQLIKFTRCNLESSLKHYRVGGTEWENAHGADNIDNPQMCIKRLVKGVYRPKQLKED
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RKQEYPKTVTSNCVSSSNFSLQSITNAIKSRMMTDHTCENISVLEGAKSQLLEFRNLN
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LPIPDRDLLLIRLPKDVPPFPQKLGFRQPEKGERICMVGSNFQTKSITSIVSETSTIM
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LHTI EAHEWVKHWKYNTSAI SWGSLNI QAAQPSGLFKVSKLI SDLDSTAVYAQTQQNR
WMFEQLTGNI KAVAHCPSQLVTKHTVKGKCQMPDLYLKLHDEAREY FQPMLGQYQKSK
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LPDGWVYCDADGSQFDSSLSPYLINAVLNI RLGFMEEWDVGEVMLRNLYTEI VYTPI S
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SDVAEAYI EKRNQDRPYMPRYGLQRNLTDMSLARYAFDPYEMTSRTPIRAREAHIQMK
AAALRGANNNLFGLDGNVGTTVENTERHTTEDVNRNMHNLLGVQGL"
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                                                                                          organism="Turnip mosaic virus"
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1181. .2554
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                                                                                                                                                                                                                                                                                                                                                                                     /codon_start=1
/product="polyprotein"
/protein_id="BAC79401.1"
/db_xref="GI:33146235"
                                                                                                                                        'moī type="genomic RNA"
'isoīate="PV376-Br"
                                                                                                                                                                                                                                        db_xref="taxon:12230"
location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CUUUCAGGCGUAAAAGGAGCCAAUUGGCAAGUAAAUUAUCCAGUCUUCAUAUCAAAUUUC 1855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1556 UGAUCAACAUGACCCACUACAGUGAUGCAGGUUUGAGUUUUUGGAAAGGUUUUGAUCGUC 1615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1496 UVAGGGGUAGCAUGGAUGGCAGAAUVAUUGACGCUCGUUCAAAGAUCACACACAGGGUUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1616 AAUTUNAUUGACAUUCGAGAUAGACCUAAAGAACGCUCAUGAGGUGCAAGGCCACUAUAAACG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1676 UNGAGGAGUGUGGCGAAAUGGCAGCCAUUGUAAACCAACUCCUAUUUCCAAUGUGGAAAA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 22.7%; Score 2309.8; DB 14; Length 9798; Best Local Similarity 41.3%; Pred. No. 0; Matches 3511; Conservative 1238; Mismatches 3557; Indels 105; Gaps
                                                                                                                                                                             product="NIa-VPg protein"
                                                                                                                                                                                                                product="NIa-Pro protein"
                                                                                                                                                                                                                                                    /product="NIb protein"
8723. .9586
/gene="CP"
                                                            /product="6K1 protein"
1776. .5707
                                                                                                                                         product="6K2 protein"
                                                                                                                                                                                                                                                                                           product="CP protein"
5. .1180
                                                                                                    product="CI protein"
                          product="P3 protein"
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/172. 872
                                                                                                                                                                                          6443. .7171
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                                                                                                               5708. .5866
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /gene="NIb"
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9590. .9798
                                                                                                                                                                                                                                                                                                                                                         .3619
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3776. .5707
/gene="CI"
5708. .5866
/gene="6K2"
5867. .6442
                                                                                                                                                     . .6442
                                                                                                                                                                                                                                            gene="NIb"
                                                gene="6K1
                                                                                                                                                                                                                                                                                                                     gene="P1"
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3620. .377
                                                                                         gene="CI
mat_peptide
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1398 CCATGAAGCACAGGTTGACACAGTTACGTGATGTCATTAAGTCTAGTTATCCACGGTTTA 1457 1856 CUUACGUGGAUCAUUUUCUUAAUCGAUAUGAGAAUAGUGAAUCGGAUGAACAAACU 1915	1916 UCGAUGCGCACAAACAAAUUGCACAAAUUAUUGGCAGUGGCAAAGAGAUUCCUUUUUCAA 1975 1518 ACCAGGATTTCGCAGAAATCCAGAGATAAGCGATGGAGTGGAAAAAGCTGCCAC 1577	1976 AUUUAGAGCAUCUGAAUGAAUUGCUAAUUAAGUCGGAUAAACCUGUUAGCGAGGAUUUCU 2035 		UCAAGAAGGGAGAGAUUCACCAUUUCCGAAAUAAGAUGUCAGGUAAAGGAACAAUUUAAUU	UUGCAUUGAUGUGGAGAACCAACUUGACAAAAAUGGUAACUUCGUGUGGGGGUGAAAGAG 	2216 GUUAUCAUGCAAGAGGUUUUUCUUAAACUUCAUUGAGAAAGUUGAUUCAACUGAGGGUU 2275	AUAAGAAACACAUAAUGCGAGUCAACCCAAAUGGCACAAAGAACAAACGGAAAAC	1878 ACACTCAGIACGAAACAAGAATAGIACCAAATGGAITCGCGGAAAGCTIGGAATGGGIAAAC 1937 2336 UGAUUUUAUCGACGGAUCCAUCUACGCUACGAAAAGAAAG	GAGUUCCAGUUGGUAAAUAUUGUACAAGCAAAAAAAAGAGAGGUUGUUACGUCAGCAU : ::	1998 CGIATCCAAITACAGITGAGIGGGIGAGCAAGICACAAGGIGATTITGICCAIGCAIGIT 2057 2456 GCUGGUGACAAAGGAAGAGGGAAGGACCAAUGGUUUCUGAUAUCAAGAGACCAACUAAGA 2515 11:1:1-1	AUCAUCUAGUCAUUGGAAAUUCAGGAGAUCCCAAGUAUGUGGAUGUACCAAGGAGCUCAA	GUGACAUGAU UGUGGCUAAGGAAGGUUAUUGUUAUCUCAACAUUUUCUUGGCAAUGU	2633 UGCUGAAUGUGAAUGAGAGUGAAUCAUCACAAAGAAGAAGAUAGAGAUAAAUG 2692	UACCGCGUCUCGGUCAAUGGCCAAGCUUAAUCGAUGUUGCAACUGAAUGUUACUUCCUAU :	TTAGCGAACTTGGTAAATGGCCCTCTCTGCTAGACGTGGCGACTGCCTGTTATTTCTTGA CAGCCUUCCACCCUGAAACGAAAAUGCUGAGUGCCCCCGAAUUCUAGUGGAUCAUACAU ::	2358 AAGTGTTCTATCCAGACGTCGCTAACGCTGAGCTACCACGCATGTTAGTGGACCACAGG 2417 2813 CAAAAUGUAUGCAUGUGAUCAUAUGGCUCGCUAGACACGCGAAUUCAUGUCÜGA 2872		2873 AGGCAAAUACUGUAAGUCAGCUAAAUUCGCCGAUAAUGACUUGGAUUCGGAGCUGA 2932
Db 13 Qy 18 Db 14	Oy 19 Db 15	Qy 19 Db 15	Oy 20			Oy 22		Oy 23		Oy 24			Oy 263.			Db 23		Qy 28 Db 24

2837 3331 3451 ACGACUDAAAGUGGUUGGAAAAAUWACAAGAAAUGUGGCGAUWAUCAAAGUACUCAAWAU 3511 GUUUGAUUCUCAGCAUTUGGCAUTUCAGCUAAUUCUAUAUCGUUCGACUAUGCACAAAUGA 3811 AGAGAGAAAAGCAGGUGA - - AUAUCGAGAAAAGUUCUGAUGAAUAAUUUAGUGGCCCUUCA 3869 UAAGGAGCAGAUAAAGAUCAAUCAG-ACCUGACAAAGGAAGAAUUUAAGGAGUACAUUG 3928 CAAGAAGUAGACCUGAGCUGAUUGCAUUAGUUAAUAAAGAAUUGCAAGAAGAAGAAGUUGAUC 3988 ----GACCUCCAUAGCAAGCAAG 2971 ANGCAUTGAGGAAGAGCCUTUTUTUGUTGAUTUTUAGCGUGUAUCUCACCAGGUGUTUTAU 3091 AGUCUGUCGCUGCUUNAUUNGCAAUGAUCCAUGGACUAGCUGCAAAAGUAACAGUUGCUC 3211 UGGCAAAUCGUAGAGACAUGAAUUCCACUCUUGAUCUCGCCGGAUUCAGCAUAUUACAAU 3391 recriciscacareceaegasceaacitatgaacitecaaacegeggataracaacitesa 3017 || | || || || || GAGATCACAGTATCTTGAAAAAGTTATCTGCAGAACCTTGGACGAAGCATGGA 3077 CUGGGAUAAGUCAACUUUCAAUGAAAGGCGCUACCGAUUUAGGCGGUCGAUAUUCAGUAU 3571 CUGCAAAGCAGUUUAUAACAUCAGUGAUGAAACCUGUCAAGAAAUCUUGUGUAAAAGCAA 3631 GAGAUACUUGUAAGGAAGUAAUCAUCAAUACAACAUCCUGGACAUUUCGGGCAACAUUUU 3691 CTAATAAACTGCGTAGTATGTCGTGGACCAGTAGCAAAGTTTCAAATAGTGTTTGTA 3317 CUTUGUGUAGUGGUGCUUGCCUGAUUGUTUGAAGUTUAUAAACAUGCUUAUAGUUAUAA 3751 agcregacarreaagaaacegaceaceaagaarceagregegaacregearreaceacr 3497 : ||:::::|||:||: TGGCTTTCTACAATAGTGGTTCACTAGAATACTTAATGAACCATTATATATTGGAGCAGATA UGGAAACCAUACACAUGACAAGCCAUUCAUACCAACCCGCGCUUCUUCAACUACAGGUCA CUGAAGANAGUAUGGAUGGAAAAAAGUUAUCUCAUGGAAUUAGAGGAUUCGUGGA CAUTAUTUAGUAGGUGGA

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5775 ATGTGCTGGTCATTTGCGGAGTACTTGGAGGAGGAGTATGGATGG	AAUCAAAGAAGAAGAGAGUUCAUCAUGAAGGAAAGGA	5835 GCTCAAAAATTTCTGAGCCCGTAACTCATGAGGCGAAAGGCAAAGAGACAAAGAAC 5894	6233 UUNAAUUUCGGAAUGCUCGCGAUAAGAAANGGGUCGAGAAGUAUAUGGAGACGACGGUA 6292 : ::: :	CUAUUGAACAUUACGUUGGAUGGCAUACGUCAAGAGGGGGGGG	CCATAGAGCATTICITIGGAGAIGCCTACACAAAGAAAGGAAAG	6353 GAGGAAUGGGCGAAAAAUCAAGACGUUUCGUUAGUAUGGUAUGGAGUUAAUUUAGAAGAAU 6412 	6413 UUGCUUUVAUVAGAUAÇAVAGAUCCAVAACUGAGCAACGCGUGAUGAGAGUCCUUUGA 6472	6075 TCTCTGCAGTTAGGTTCGTAGATCCACTCACAGGAGGACCACTAGACGATAACCCATTCA 6134	6473 CAGAUGUGGAAUUAGUGCAAGCUCAUUUCGGAGAAAUCAGAGACAAAAUGCUAGACGAGG 6532 :	6533 GCCUCAUCGAUAGGCAACACAUCUUAAAUAAACAGGUUUGACAGCAUACUUAGUUAAGG 6592	6195 ATGAACTGGATCCAAATGAGATACGAGTGAACAAGACAATCCAGGCATACTACATGAACA 6254	6593 ACGGGGUVAAGUCAUGAAAGVAGAUUVGCAACCACACAAUCCUCUACUAUAUGCA 6652 	Jaaacaaagcgacaabaagcagguuuccugagaaggguuguuuguuugggacaaaagggaca	6315 ATCTTCACGCAACCATTGCTGGATTCCCAGAGGGAAAACGAACTGAGGCAGGC	6713 AAGCAUAUGAAGUAAGAAGAAACUACCAGAACGAAAGAACGUUU 6763 	CUUUUGAAGGAGCUCAAGUGUGAAGGAAUUGCGCGAUUACAAUGGUGUAGCCAGCGCUA	6435 ACCATGAGAGCAACTCCATGTTCAGAGGACTGGGGGACTACAACCCAATCTCGAACAACA 6494	6824 UUUGCCAACUCAAAACUCAAAUGGUCGGUCCACACAACUUAUGGGGUUGGCUUUG 6883 :::	GCUCAUACAUCAUAGUAAUAGGCACCUGUUUAAAGAAAAUAAUGGGAAUUUAUUGAUCA	GACCACTCATATTAACGAACCGACATCTCTTTGAGCGGAACAATGGCGAGCTTGTGATAA	6944 ANUGGACGANGGANDUCAANAUUCAGAACUCCAAAANAAAAGAGGGGGGGGGGGG	1004 AGGAUAGGGAUAUGCCAUUCUUCAAAUGCCUAAGGUUCCCACCCUUUGCACAGGGU 1063	6675 CAGATAGAGATCTTTGCTAATCCGATTGCCAAAGGACGTCCCACCTTTTCCGCAGAAAC 6734	UACGAUTUVGGAAAUCCAAUAGUGGGGGAAAUCAAUTUGUCUUGUUGGAAAUACGUUCCAAG		7124 AAAAGUACAAGCAUCGUUGUGAAACAAGCAAAACAUCCCACGAGUUGAAGGUA 7183		6855 AATTTTGGAAACTGGATTAGCACTAAAGACGGCCAATGCGGAAGTCCAATGGTGAGCA 6914
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7543 7423 7544 AUTUGAAAGCGGUUGCAACUAUUCCCAAUAACUTUGUUACAAAGCACAUUGUGAAAGGAC 7603 7271 7663 7783 7451 7843 7903 7963 8023 7691 8143 7811 7424 AGGAUAGUGCUCCAUGCAAAGAAUUCAAAACAACUAAGUUGAUUAGCGACUUAUGCACGG 7483 7331 7511 7571 7631 7871 8263 7931 8323 8144 UNAAUANGAAAUGCCCAUGGACAGUCGGGAUGACUAAGUUUVAUUGCGGAUGGAAUGAUC 8203 7991 7604 GAUGUAAAUUGUUUGAAUUGUAUCUGCAAACUCGUAGUGAAGCGAAUGAGUUCUUUAAAC 1484 AACCUGUGUGCGCUCAGAGUAGCAAUCAAGUUAGAUGGUUAUAUAAUCAGCUUGAAGGAA 7304 AUTUCUCGAACUUUGACGACGCGUUUGAAGGCGAUUAUAUUAAACAAGUUGAAGGAACUGA 7364 AAUGGGAGCAGAAUUGGACUUACAACGUUAAUACUGUUAGUUGGGGCAACAUGAAACUUC 7724 UNAAAUACUCAUCAGAAAUACCAAUUGGGGAGGUCGACACUGAGAGAUTUGAAGAUGCAG 7784 UUGGGCAAGUCAUCGAAAUUAUGAUGCAAUGGAACUUUAGGGAAUGCAAGUAUAUCACCG 7844 AUUGUGACCAGAUCUUUGAAUCAUUGAACAUGAAAGCGGCAGUCGGUGCGUUGUACAGUG 7904 GUAAGAAAAAGGCGUACUUCGAAAAUUCCACAUTUGAUGAUCGAAAAUCAUTUGCUACAGC 7964 UNAGUIGUCUCCGAUUAUUCAAGGGIGAUUUGGGAAUTUGGAAUGGAAGUCUUAAAGCUG 8084 UNGABACUTUACUTGCCGGABAGGUTUGCGUCGAUGAUTUCCBACAACCAAUTUTAAUGAUC

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Turnip mosaic virus gene for polyprotein, complete cds, isolate:Al.
AB093598
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                             8232 TACTGCTAAGCGTACACAGAGTACGAGTATATCCTTGACACTATGGCAGACAACTTTC
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         AUUGGGACAUAGGCGUGCAGAUGCUUCGAAAUUUGCACACUGAAAUAAUUUACACCCCCA
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QSVLAQLQVIERSLPELVEARANIVGPDSAASQACNKFLGMLIHMSEPNNELASGGYT
ILRDHSITILBKSYLQILDEAWSELSWSBRCAIKYYSSKQAIFSQRDLPMQSGVDLGG
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VOLVGISLITITASEANRI VTAQRKLADVAFTERKKT WEBLARHSTLITHSANDHPT
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SGFALNYFANNRARIEEFDFVIFDECHVHDANAMAMECLLHECDYSGKIIRVSGTPS
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ATGEEFEQATKHLLEITRYMKNRTENIEKGSLKSFRNKISQKAHINPTLMCDNQLDKN
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GDPKYVDLEPEBENKMYIAKEGYCYINIFLAMLVNVKESQAKEFIKVVRDKLVGELGK
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VEQLIKFTRQNLESSLKHYRVGGTKWEDTHGANNIDNPQWCIRRLIKGYRPKQLKED
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LLARRDPKYTKVDGRTPKKVAN IEITTSGTPSKGFIVANTI IENGVTIENGSTLDDVADFGT
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TEAALKCFTYGLPVITNNVSTSILGNVTVKQARTMSVFEITPFYTSQVYRYDGSHPRO
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DKMQI I LINGLMVWCI ENGTSPNINGMWVMMDGDDQVEFPI KPLI DHAKPTFRQIMAHF
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VIRGEHEGKLYDARIKVTRTISHKIVHPSAAGANFWKGFDRCFLAYRGSDREHTCYTG
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Best Local Similarity 40.8%; Pred. No. 0;
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5244 GAGAAUUGGAACUACAAUUAAAGGAUUG 8104 UGCAAUUCAAUGCCACACAGAAAGGTTTC 8104 UGCAUUUCAAUGCUUCACAUUGGAUUG 8105 CGCTCTTAAATGCTTCACATATGGACTT 8105 CGCTCTTAAATGCTTCACATATGGACTC 8106 UUUAUCAAUUGCAGCAGUCCAGCCAGCC 8107 CTTGGTAACGTCACAGUCAAGCAGCC 8108 CGCTCAAAUGCAGCAGAGCAGCCAGGCC 8109 TCTTGGTAACGTCACAGGAAAGCAAGAAGCAGCAGCAGCAGCAGCAGCAGCA		•	5773 AGATGTATTGGTCATATGCGGCGTTCTTG180 CAAUCAACAUGAAGAA 5833 GCAATCTGGTATTACGGAGCCCGTTACTG231 GCUUAAAUUCGGGAUGCUCGCGAUAACG31 GTTGAATTTCGCAATGCTCGAGACACCGGA
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4167 AGACAUCUUGACUGACAAAGAAACCACUUGAUUUCGACUUAGAUUGUGAGGGAGCAA 4226	4584 UAUAUGUAUAAUGACUAGUUUGCUUUCAAUUACUUUGCAAAUAAUCCUCUAAAAUU 4643	ACAACUUAGUUCCAAGCUUUUGUGAAGCACCAGAGUCUGGGUCUGCAGGGUGUAAU L:: :: :	
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5412 5303 5292 5352 6029 5712 5832 6230 AGAAAAUGGGUCCAGAAGUAUAUGGAGACGACGG 6290 || |:|||: ||||| :|:||||| ||| CCAAGATGGGTAGAGACTCTATGGAGATGACGA 5952 JGCCUGUAAUGACACAAGGAGUUUCAGUUAACAG 5363 AAAUUCAAÇUUAGUGCCAUGGÇUUUUAACUUUAC 5543 AAUUUUAUGACAGUAUAGGAAUCCAUCUUGAUUU 5603 AUUGUAGAGAAUUCÇÇAGAUAUGAAAUACÇGACA 5663 AGAGCAUAAAUUGUUUUGUAGAAUGAGUGUUGU 5723 JUAAAACAGACAUUCAUUCAAUUGGAAAAACUCU 5783 AAGAAUAUAGAAACAGCAUCAUUUUAAAGCAAU 5843 CUGGCAAUAUUCAGAAAUUGCAGGCAGCAAAGAA 5963 AUCUUGAUCCUUCGGCGA------ 6007 |: || | ::|| | Argental | Argensore | : : | | Argensore | Argensor CUAUUGGUGGUUUCUGGAUGAUAUGGGAUAAGUU 6179 CTCATGAAGCAAAGGCAAGAGACAGAGACAAAA 5892 CAUACGUCAAGAGGGGCAGUUAAGGGCCAGAA 6350 :| | : || GTGAATACGCTCGACTTGGTGCAAATGTTGAGGA :|:| || : ||||| | TGTGTCGTGACATTCCAGAAAACTCCATCTAGA : ||||||| : | :| |:: | ||| : rgcaacagatgtcaactctattcaacgaacagt : | | | : | | | : : | | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | | : : | : : | | : : | : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : | : : : | : : | : : | : : : | : : | : : | : : | : : | : : | : : | : : : | : : : | : : : | : : | : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : : | : : JGAUJGAGAUJCCUAGUCUJGUGGCGACACAGGC | || :::| | : AAGGCGACGCAGGCTTTTCAAGCGC regenecutivacina cun activa con con activa co -GUUCAUCAUGAAGGAAAGAGAAGACUCAAAA

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Submitted (11-OCT-2002) Kazusato Ohshima, Saga University, Faculty
Submitted (11-DCT-2002) Kazusato Ohshima, Saga University, Faculty
Saga 840-8502, Japan (E-mail:ohshimak@cc.saga-u.ac.jp,
Tel:81-952-28-8730, Pax:81-952-28-8709)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Turnip mosaic virus
Turnip mosaic virus
Viruses; ssRNA positive-strand viruses, no DNA stage; Potyviridae;
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                                                             UGAAGCAUACAUCGAAAAGAGAAAUUAUGAGAAGCCAUAUAUGCCGAGGUACGGUAUUCA
                                                                                                                                                    <u> AAGGACGCCAGCUCGGGCCCGGGAAGCCCACAUCCAGAUGAAAGCUGCAGCAUUGCGAGA</u>
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                                                                                                   <u>ACGGAACCUCACCGACAUGAGUUUGGCGCGAUAUGCUUUUGAUUUCUAUGAAAUGACAUC</u>
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22745497
12859632
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Turnip mosaic virus gene for isolate:St48.
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VVCVSLLITTASEANRIVAGNKRKLDVAETERKKKTEMEAFHSILTGTSANDHPT
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               )5. .1180
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1529 GCAGAGATTCAAAGCCTGACTGATGGAATGGAAAAGCAGCATTCCGCATGCAAAAAG 1588

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CAUTUTUCUTAAUCGAUAUGAGAAUAGUCUGAAUCGGAUGAACACAAACUUCGAUGCGCAC 1926
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Matches 3523; Conservative 1268; Mismatches 3770;
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                             /product="NIb protein"
8723. .9586
/gene="CP"
                                                                           product="CP protein"
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//gene="P1"
1181. .2554
//gene="HC-Pro"
2555. .3619
//gene="P3"
3620. .3775
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172. .8722
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ò	2047	CAAUGCCUUUUAGAGCUAAACGCUGGCAUAAAAACAGGAGCGAUUCAUUC
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ò	2107	GAGAUUCACCAUUUCGGAAAUAAGAUGUCAGGUAAAGCACAAUUUAAUUUUGCAUUGAUG 2166
qq	1709	:
à	2167	UGUGACAACCAACUUGACAAAAUGGUAACUUCGUGUGGGGGGGG
Db	1769	:
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Д	1829	AAAAGATTCTTCAGCAACTACTTTGAGATAATTGATCCAAAGAGGGCTATACCCAGTAT 1888
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Ωp	1889 (SAAACAAGACTAGTGCCAAATGGTTCTAGGAAACTTGCCATTGGAAGCTCATAGTTCCA 1948
ò	2347	ACGGAUCCAUCUACGCUACGACAAAUGAAAGGUAGCCCAAUCACAGAGUUCCAGUU 2406
οp	1949	acaaaititicaggiititaaggagagaaaataaaggaggaggagagagag
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Ор	2069	ACTGAATCAGGCGATCCGGTTTTATCAGAGATCAAAATGCCAACCAA
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Dp	2249	
È	2704	GGUCAAUGGCCAGCUUAAUCGAUGUGCAACUGAAUGUUACUUAC
qq	2309 (
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È	2824	CAUGUGAUCGAUUCAUAUGGCUCGCUAGACACGCAAUUUCAUGUUCUGAAGGAAAUACU 2883
q _O	2429	
ζ	2884	GUAAGUCAGCUAAUUAAAUUCGCCGAUAAUGACUUGGAUUCGGAGCUGAAACAUUAUUUA 2943
qq	2489 (
ò	2944 (GUAGGUGGAGACCUCCAUAGCAAGCAAGCCAGGGGGGGGGG
qa	2549	
&	2983	UCCAUAAAUUACUCUGUAAAUGUAUAUAUAGCCCUAAAUUGAUGAGGCAAUGCAUUGAG 3042
qq	2609	TGTATCAAGAGACTTATACTAGGTGTGTTAGGCCGAAGCAACTAAAGGAGGACATATG 2668

3088 3882 3939 4119 3745 3282 3702 3269 cecaacaerererereaereaereaeaaaarareraecaecarreeeeeaecarcaar 3328 3625 2669 GCCAACCCTTTCTTACCACGTATGCTTTACTCTCACAGGAGTTATTGGCATTTTAC 2728 2729 AACAGCGGCTCTCTAGAGTACTTGATGAACCATTACATCAAGGCAGATAGCAATATTGCC 2788 3403 AUGUAUUGGAUGGAAAAAGUUAUCUCAUGGAAUUAGAGGAUUCGUGGAACGACUUAAAG 3462 UGGUUGGAAAAUUACAAGAAAUGUGGCGAUUAUCAAAGUACUCAAUAAUCUGGGAUAAGU 3522 AGCAUTUGGCAUTCAGCUAAUTCUAUAUCGUTCGACUAUGCACAAAUGAAGAGAAAAG 3822 GCCACAUGUGAUGAACCUGUCGCACAUCAAAGCUUGGACGACAUUCAAGACAUCUUGACU 4179 3043 GAAGAGCCUUUUUUGUUGAUUUUUUGGGGGUGUUUUAGGCUUUAUUAGCUUUAUAUU 2849 GCTCAACTCCAAGTCATTGAGCGAAGCTTACCGGAACTTGTTGAGGCTAAGGCTAATATC 2909 ACAGGACCAGATTGTGCAGCCTCTCAGGCATGTAACAGATTTTTGGGTATGCTCATTCAC CAACUUUCAAUGAAAGGCGCUACCGAUUUAGGCGGUCGAUAUUCAGUAUCUGCAAAGCAG CCUGAGCUGAUUGCAUUAGUAAUAAAGAAUUGCAAGAAGAAGUUGAUCAUCAAGCUAAG GCUTULAUTUGCAAUGAUCCAUGGACUAGCUGCAAAAGUAACAGUUGCUCAAACAUUGAAU 323 GAGCAGAGACUAAUACUUGAACGCGGGGCGCGCAUUUGAUUUCGGUCAUGGAAACCAUA 3283 CACAUGACAAGCCAUUCAUACCAACCCGCGCUUCUUCAACUACAGGUCAUGGCAAAUCGU AGAGACAUGAAUUCCACUCUUGAUCUCGCCGGAUUCAGCAUAUUACAAUCUGAAGAUAGU UUUAUAACAUCAGUGAUGAAACCUGUCAAGAAAUCUUGUGUAAAAGCAAGAGAUACUUGU 3643 AAGGAAGUAAUCAUCAAUACAACAUCCUGGACAUUUCGGGCAACAUUUUCUUUGUGUAGG UGGUGCOUGAUUGUUUGAAGUUUAUAAACAUGCUUAUAGUUAUAAGUUUGAUUCUC 3389 Accaracerrengaceraarcecarnerracacecaaagaagrrraagacerr 3823 CAGGUGAAUAUCGAGAAAGUUCUGAUGAAUAAUUUAGUGGCCCUUCAUAAGGAGCAGAUA 3883 AAGA---UCAAUCCAGACCUGACAAAGAAGAAUUUAAGGAGUACAUUGCAAGAAGUAGA UUUGACUCAGAGAAAAGUGAUUGUGUAUAUAAAGACACUGAACAAAUUGCGAAAUCUCGUU 3343 3463 3523 3583 3763 3509 3940 4060 4120 3103 3163 3703 셤 8 8 ઠે 음 중 음 8686 \$ B \$ g 8 6 ⋧ d 8 6 ð 8 8 8 8 6 8 6 상 음 상·음 8 쉽 ð

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	UUCUAUGGGAAGAGGGGUCUCAACAAGGAAGCAUACAUUAAAGGACCUAUUUAAAUACUCA 7734		UGCCCAUGGACAGUCGCGAUGAAUUUGUGGGAUGGAUGAUCUUCUAGGUAAA 8214 GCTCCCTGGAGTTGTTGTTTTTTTTTTTTTTTTTTTTTT
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   TGGGTGATGATGGATGGTGATCAGGTGGAATTCCCGATTAAACCGCTCATCGATCAC 9238
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                                                         CGGCCCCGGGAAGCCCACAUCCAGAUGAAAGCUGCAGCAUUGCGAGAUGCGAAUAAUAAG
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                                       GCAAAAACCCACUUUGCGUCAGAUUAUGGCUCACUUUAGCAAUGUUGCUGAAGCAUACAUC
                                                                                                           GAAAAGAGAAAUUAUGAGAAGCCAUAUAUGCCGAGGUACGGUAUUCAACGGAACCUCACC
                                                                                                                              GACAUGAGUUUGGCGCGAUAUGCUUUUGAUUUCUAUGAAAUGACAUCAAGGACGCCAGCU
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(Dases 1 to 9741)

Maiss, Timpe, U., Brisske, A., Jelkmann, W., Casper, R.,

Mattanovich, D. and Katinger, H.W.

The complete nucleoride sequence of plum pox virus RNA
J. Gen. Virol. 70 (Pt 3), 513-524 (1989)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:12211"
/clone="ppv-NATf[274, 31, 47, 232, 65]"
colone="ppv-NAT genome excluding the 3' poly-A
tail-propagated in Nicotiana clevelandii"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
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Plum pox virus genomic RNA, complete genome.
D13751 D00424
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Plum pox virus
Viruses; ssRNA positive-strand viruses, no
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/db_xref="G1:222409"
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/isolate="PPV-NAT"
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8575 AUCAAUCCAAAAUUUAUACACAUCCUAGAUUCUUUVAAAGUUCAUUUUGCUAAUUUAGGU
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ESIYOBELQEHFSQCJGLNYTFTKTENKEELMFNSHKGYLYDDWYIPKLEPERIYSILE
WDRSNEPPLAYDDYNLAMTYSKELLREINKEYSWVLEQDMYIPKLEPERIYSILE
WDRSNEPPLAYDDWIAMTYSKYELLREINKEYSWVLEQDRYNALSKOGKAPYIAE KGGMMSAQDY I EASDHLRELARYQKNRTENI RSGS I KAFRNKI SSKAHVNMQLMCDNQ LDTNGNFVWGQREYHAKR FFRNY FDV I DVSEGYRRH I VRENPRGI RKLA I GNL VMSTN IIRLPKDFPPFPRRLQFRTPTTEDRVCLIGSNPQTKSISSTMSETSATYPVDNSHFWK HWAISTKOGHOULPIVSTROOSILGHELANSTWYDNPYAPEPDNFETTYLSNQDNDNW IKOMRYNDDBVCWGSLOLKRDIPQSPFTICKLITDLDGEFVYTOSKTHWLRDBLEGN LKAVGACPGQLVTKHVVKGKCTLFETYLLTHPEBHBFFRPLMGAYQKSALNKDAYVKD LAALRKQLLGEECIHFEVSKECTSKRGENFVYQCCCVTHEDGTPLESEIISPTKNHLV TALKKLYTDTEASETEIERYLEAFYDNINDDGESNWWHQADEREDEEEVDALQPPPV IQPAPRTTAPMLNPIFTPATTQPATKPVSQVSGPQLQTFGTYSHEDASPSNSNALVNT NRDRDVDAGSTGTFTVPRLKAMTSKLSLPKVKGKAIMNLNHLAHYSPAQVDLSNTRAP QSCFQTWYEGVKRDYDVTDDEMSIILNGLMVWCIENGTSPNINGMWVMMDGETQVEYP IKPLLDHAKPTFRQIMAHFSNVAEAYIEKRNYEKAYMPRYGIQRNLTDYSLARYAFDF YEMTSTTPVRAREÄHIQMKAAALRNVQNRLFGLDGNVGTQEEDTERHTAGDVNRNMHN LLGMRGV"

1730 GGAAAAUAACAUGCACUCAAUGUGGAGAACUGCUUGAAAUGUUGUCACAAGAAGAGGAAC 1789 AGCAGAGCAATGAGATAATCCACTACTCAGACCCAGGCAAACAATTTTCGGATGGTTTCA GCGUUAUGAUCAACAUGACCCACUACAGUGAGGCAGGUUUGAGUUUUGGAAAGGUUUUG AUCGUCAAUUUAUUGACAUUCGAGAUAGACCUAAAGAACGCUCAUGAGUGCAAGGCCACUA UAAACGUUGAGGAGUGUGGCGAAAUGGCAGCCAUUGUAAACCAACUCCUAUUUCCAAUGU TTATAGTTCGTGGAAAACACACTCTATTCTTGTTGACTCACGGTGTAAGGTTTCTAAAA CCAATTCATTTATGCA---GTGCAAGCTACGGAAACTGATCATCAGTGCACATCTGACC Length 9741; Best Local Similarity 40.1%; Pred. No. 0; Matches 3422; Conservative 1319; Mismatches 3689; Indels 104; Score 2303.6; DB 14; Pred. No. 0; :: 22.7%; 9649. .9653 polyA_signal ORIGIN 1490 1550 1045 1610 1670 1105 1162 Query Match a g ઠે 셤 a ሯ ઠ ઠે ઠ

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8955 GACTTGTCAAACACGAGGCTCCGCAGTCTTGTTTCCAAACTTGGATAAAGAGTTAAG 9014
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Plum pox virus isolate SoC polyprotein mRNA, complete cds.
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Location/Qualifiers 1. .9795 /organism="Plum pox virus"

source

FEATURES

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CTSDLDVQEGGYVAALVCQAIIPGGKITCLQCAEKTAYMSQQBIRDRESTVIEQHEKT
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KGGMYTVQDYSEASDRIRELARYQKRNTEHOOSGSIKAFRRIKISAKAHVMQLMCDNQ
LDTNONFVWQQRETHAKRFPRNYFNVIDTSEGYRRHIVTRENPRGARKLAIGNIVMSTN
LAALRKQLLGEECTRFEVSKECTSKRGANFVYQCCCVTHEDGTPLESEIISFTKNHLV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                KLGTWPSMMDLATACHFLAVLYPETRNAELPRILVDHESKIPHVVDSYGSLSTGMHIL
KANTYNQLISTBOPTIDSSMGYYLVGGLEVDRODEPROVKLILRSIYREBEMQQVLTB
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NAQMVVIDEHASVLHDSVFNGTKPYASYVMAIKTLERMKARTESDHTLHDLGFSVLRN
                                                                                                                                                                                                           KLKQQYKEERERFQWINGPENVVTHI EPVTEEAPTWVPFPDVPKRPLSKTPSMKRHII
FDKVRMSETTLQLFMRRVANNAKANGQKVEI I GTKHVVGNY I RKSQLTYFRTHVRHLD
GLKPRYD I TLDEATKKI VQI FANTSGFKHVHGKGE I TPGMSGFVI NPRNI SDPMQIHD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    DADGSQFDSSLSPYLINAVLNIRLAFMEKWDIGEQMLSNLYTEIVYTPIATPDGTIVK
KFKGNNSGQPSTVVDNTLMVILAMTYSLLKLGYHPDTHDCICKYFVNGDDLVIAVHPS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ETALKKLYTDEEASETEIEKYLEAFYNNAGDELDSNIVVHQAKEGNDDGVTLVDAGKS
TVTTAVSTPAVTSSQFPPPFFPNLQSTAPMFDPIFTPATTQPNVRPIAPVVTSPFSYG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ningmavmmdgetqveypikplildhakptprqimahfsnvaeayiekrnyekaympry
giolnitdyslaryapdfyemtsttpvrareahiqmkaaalrnvqnrlfgldgnvetq
eedterhtagdvnrnmhnllgvrgv"
                                                                                                                                                                                                                                                                                                                                                                                                                                           I GNSGDSKYVDL PKTEGGGMY I AKAGY CY I NI FLAML VNVNEGEAKS FTKTVRDTL V P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EWDRSHEPIHRLEAICASMVEAWGYGDLLMEIRKFYSWVLEQAPYNALSKDGKAPYIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             VI GNONVT PSSSNALVNTRKDRDVDAGTI GTFSVPRLKSMTSKLSLPKVRGKA IMNLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HLAHYNPAQTDLSNTRAPQSCFQTWYEGVKRDYDVSDDEMSIILNGLMVWCIENGTSP
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/db_xref="taxon:12211"
147. .9578
                                  CDS
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1609 Db 2122 CAATGCTCGTTAATGTTAA 1104	2687	2747					3047	2089 3107 GUCAGCADUDASABUAGC 2089 1: 11		2209 3227 AGAGACUAAUACUUGAACG 2009 3227 AGAGCUAAUACUUGAACG	δ d	2329 Oy 3347 ACAUGAAUUCCACUCUUGA 2329 Db 2842 AATCAGATCACACTGCA 1821 Db 2842 AATCAGATCACACTGCA	& a	ራ ብ ‹		3587		2686 Qy 3707 GCUUGCCUGAUUGUUGAA : :::
1550 GCGUUAUGAUCAACAUGACCCACUACAGUGAUGCAGGUUUGAGUUUUGGAAAGGUUUUG :		1670 UARACGUUGAGGAGUGUGGCGAAAUGGCAGCCAUUGUAAACCAACUCCUAUUUCCAAUGU :	1730 GGAAAAUAACAUGCACUCAAUGUGGAGAACUGCUUGAAAUGUUGUCACAAGAAGAAGGAAC 1730 GGAAAAUAUGUCACAAGAAGAAGAACCUGCAAGAAGAACTATGCATGTCACAGCAAGAATGCCAGAAAGTATGCATACATGTCACAGCAAGAATTC	1790 UUGAAUCUUUCAGGGGUAAAAGGAGCCAAUUGGCAAGUAAAUUAUCCAGUCUUCAUAUCA 	1850 AAUTUCCUUACGUGGAUCAUUUUCUUAAUCGAUAUGAGAAUAGUCUGAAUCGGAUGAACA		1970 UUUCAAAUUUAGAGCAUCUGAAUGAAUUGCUAAUUAAGUCGGAUAAACUUGUUAGCGAGG :	2030 AUTUCUAUGAAAUGUCUCAAUGCCUUTUAGAGCUAACAGGCUGGCAUGAAAACAGGAGCG	AUCANUCAAGAAGGGAGAGAUUCACCAUUUCCGAAAUAAGAUGUCAGGUAAAGCACAAU 	UDABUUUGCAUUGAUGUGAGAACCAACUGACAAAAAUGGUAACUUCGUGUGGGGUG 	AAAGAGGUUAUCAUGCGAAGAGUUUUUCUUAAACUUCUUUGAGAAAGUUGAUUAAUCAACUG	2270 ACGGUUAUAAGAAACACAUAAUGCGAGUCAACCCAAAUGGCACAAGACAAACAGCUAUAGA	GAAACUGAUUUUAUCGACGGAUCCAUCUACGCUACGACAACAAAUGAAAGGUAGCCCAA		2450 CAGCAUGCUGGUUACAAUGGAAGAUGGUACGCCAUUGUUUUCUGAUAUCAAGAUGCCAA :	2510 CUAAGAAUCAUCUAGUCAUUGGAAAUUCAGGAGAUCCAAAGUAUGUGGAUGUACCAAGCA	2570 GCUCAAGUGACAUGAUGAGCUAAGGAAGGUUAUUGUUAUCUCAACAUUUUCUUGG	2627 CAAUGUUGCUGAAUGUGAAUGAGGUGAAUCAAAAAUCAUUCACAAAGAAGGUUAGAGAUA 2686
දු පු	දු පු	상 임	& 8	상 원	දු පු	දු පු	දු පු	충 <u>원</u>	8 &	상 원	9 G	දු දි	B & B	9 9	දු පු	상 원	දු පු	ò

2926 3046 3166 ACCAUTUAGGCGGUCGAUAUTCAGUAUCUGCAAAGCAGUUA 3586 CUGUCAAGAAAUCUUGUGUAAAAGCAAGAGAUACUUGUAAGG 3646 Secondala de la 1138 d CAUCCUGGACAUTUCGGGCAACAUTUUCUTUGUGUAGGUGGU 3706 TGGGGAAGCTATTCTGCAAAGCTGTCGGTCTTTCAACGAATT 3198 AGUUUAUAAACAUGCUUAUAGUUAUAAGUUUGAUUCUCAGCA 3766 2481 2721 3286 3346 UNGGUGGAGACCUCCAUAGCAAGCACCUCCUCAGUGUUCCA 2986 WAGCGUGUAUCUCACCAGGUGUUUWAUWAGCUUWAUAWAWA 3106 AUCUCGCCGGAUUCAGCAUAUNACAAUCUGAAGAUAGUAUGU 3406 UGUGGCGAUUAUCAAAGUACUCAAUAUCUGGGAUAAGUCAAC 3526 BAGCATGCATCAGTCCTCCATGATAGTGTTTTCAACGGGACAA 2781 IGUAUAUAUAGGCCUAAAUUGAUGAGGCAAUGCAUUGAGGAAG AUGUGAUCGAUUCAUAUGGCUCGCUAGACACGCAAUUUCAUG SUAAGUCAGCUAAUUAAAUUCGCCGAUAAUGACUUGGAUUCGG TTGGAGGTCTAGAGGTTGATCGATGCGATGAATTCAAGAATG CUUUAAAGUACUGGAUGAGCAAGCAACAGUCUGUCGCUGCUU GACUAGCUGCAAAAGUAACAGUUGCUCAAACAUUGAAUGAGC GUCAAUGGCCAAGCUUAAUCGAUGUUGCAACUGAAUGUUACU CUGAAACGAAAAUGCUGAGUUGCCCCGAAUUCUAGUGGAUC GCGGGGGCGCAAUUUGAUUUCGGUCAUGGAAACCAUACACA AACCCGCGCUUCUUCAACUACAGGUCAUGGCAAAUCGUAGAG

3 3 <th>666666666666666666666666666666666666666</th> <th>\$ 8 \$ 6</th> <th>8 8 8 8 8 8 8</th> <th>8 6 8 6 8 6 8 8</th>	666666666666666666666666666666666666666	\$ 8 \$ 6	8 8 8 8 8 8 8	8 6 8 6 8 6 8 8
3199 TTCTTCCAAAAGTTTTCAAGATGATTGATATGCTAATTGTGATCAGTCTTCTTTGACTA 3258 3767 UUUGGCAUUCAGCUAAUUCUAUAUCGUUCACUAAUGAAGAGAGAAAAGCAGG 3826 3259 TCGGTGCCACATGCAAATCCATGATCAATGAGCATCAGCGGCTCAAACAGATGGCTG 3315 3827 UGAAUUCGAGAAAGUUCUGAUGAAAAUUAAGGCCCUUCAUAAGGAGCAGAUAAGA 3886 3316 TCGTCGTGAAAAGUUCUGAUGAAAAAUUAAGGCCCUUCAUAAAGGGCAGAUAAAGA 3886 3316 TCGTCGTGAAAAGAAAAAAAAGGGTTCAAGCCTTTTAATGTGCAAGAGGTTACGG 3375 GCAUCCAGACCUGACAAAGGAAGAAUUAAGAGAGAAAAUUCAAGAAGAGAAAACC 3435 3376 ACAAACTTGGCTAATATGCCAACAAGGAGACTTCTTGGAATATGTGCAAAGGGGAAAACC 3435	CUGAGCUGAUUGCAUUAGUUAAGAAUUGCAAGAAGAAGUUGAUCAUCAGG 399	TCATGGGGGGGTTGATCAAACAGTGCATCATCAGAATTTAGATGACATTGAGGATATTT UGACUGACAAAGAAACAACCAUUGAUUUCGACUUAGAUUGGAGUGGAGGGGGGGG	4295 UACCCCAUUANGAAACCACUGGGAAAUUUAUUGAAUUCACUGGUGAAGCUGUUAAGGGG 4354 3796 TACCACACTACCGGACTGAAGCTCACTATGGAATTCACGAGGAAAATGCACATG 3855 4355 GAGGAAAAAGCAAGGACTGAAGGAAAAAAGGAGAAAATGCACAAGGAAAAAGCACAAGAAAAAGCACAAAAAAAGCAAAAAA	4535 CAAACCCCACAUUGAGAAUGCGAGAAUGUCAUUUUGGAUCAUAUAUAU
8 8 8 8 8 8			86868686	8 6 8 6 8 6 8 6

4695 4954 4455 5014 5074 5134 4635 5194 5254 5314 4875 5434 5494 5055 5614 5115 5674 5175 5734 5235 5794 4696 GGATTCAGCGACTCGGTCGTTGGTCGAAACAAACCAGCGCAGCATGCGAATTGAAG 4755 4936 CTAIGGICAGGITIGACGGIACAAIGCAICAGAAAITITITICGACIGITGAAGAGITACA 4995 5495 AGUUAGAUGAGAAUCUGAAAUUCAACUUAGUGCCAUGGCUUUUAACUUUACCGUAACAUCUA 5554 5236 AAATAGCCTACACACACAGACGACATACACTCCATCCCACGAACTGTCAAAATCATTG 5295 5795 ACGCCCUCUUGCAAGAAGAAUAUAGAAAACAGCAUCAUUUJAAAGCAAUGACAAGUAACG 5854 5855 CAUGUAGUGGAACACUTUTUCAAUGCUAAGCAVAGCAAAUGCAAUACGAACCACUAUG 5914 |||||: : ||:|| ||: || ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| ||:|| || S135 AAAUUGAUUACGACAACCGGUGCGUUAAUUACACAAAGACCAGCAUUUCAUACGGAGAAC 5315 GCUCACAUAUGGAUUGCCUGUAAUGACACAGAGGAGUUUCAGUUAACAGUUUAUCAAAUU 5375 gcacaguccgacaggccagaguuaugucucguuugaguugccgcccuuacuuuauggcuu 5555 UUUGGCUAGAUUGUAAAUUUUAUGACAGUAUAGGAAUCCAUCUUGAUUUACCGCGCGAAG 1895 ACAACAUTUTAGUGUAGUUGCUAGUUACAAUGAGGUUGAUCAGCUCUCAAAAAUGCUCG 4955 GAGAUAAAGGCUAUUAGUGACUAAAGUCGAUGGCCGUACCAUGAAAAUUGGUUCGACCG 5075 AGAAUGGAGUCACUCUAGAUGUAGAUGUUGUUGGACUUUGGUUUGAAAGUCACUGCUG 4636 TTCTAGACGTTGATAATCGGCTTGTGCGGTATACAAGACAAGTATCAGTTATGGCGAGC 5435 CACUUGUAUAUCAUGAUGGCAGCAUGCACCCUGAAAUUCACAAGCAUUUAAUUCCUUACA 5615 CAAAAAUUCCAUUCCAUUGUAGAGAAUUCCCAGAUAUGAAAUACCGACACUUGUGGGAAG 5675 AUAUUCUCAAAAUCAAGAGCAUAAAUUGUUUGGUAGAAUGAGUGUUGUUAGCGCAACAA 5735 AAGUAGCAUAADACUUAAAACAGACAUUCAUUCAAUUGGAAAAACUCUGGAUAUAUUG UCCAAGCUUUUUGUGAAGCUCAAGGAACUGGGUCUGCACGAGAUGUAAUCAAUAAGGGAG 4835 5195

FEATURES

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ATGERY OF THE TRANSMICTORY                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REVERSTOYPVTISTEDTLSPONFVSAQGSGSNCDVISKGDNILVYVASYNEVDTLSK
LLABRDFKVTKVDGREMKVGNIEJTTSGTPSRKHFIVATNIJENGYTLDIDVVADFGT
KLYPVLDTDNEMLSTTKVSINYGERIQRLGRVGRHKPGHARIGHTRIGHTBKGLSEVPSCIA
TEAALKCFTYGLPVITINNYSTSILGRYVTVGARTMSVPEITPFYTSQVVKYDSSMHDO
VHALLQRFKLRDSEIVLNKKLAIPNRGINAWLTASEYARLGANVEDRRDVRIPFMCRDI
                                                                                                Tomimura,K., Gibbs,A.J., Jenner,C.E., Walsh,J.A. and Ohshima,K. The phylogeny of Turnip mosaic virus; comparisons of 38 genomic sequences reveal a Burasian origin and a recent 'emergence' in east
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KROZYKTYTYSOKUSSSSFSLOSITMAIKSRIWICHTCERISIILEGARSOLLEEFRULN
ADHSFTTKTDGISRNENSEVGALEAVHHOSTNDMSKFLKLKGKWIKTLITRDVLVVCG
VLGGGIWMILORLOSGVTEPVVHEAKGKRORCKLKFRNARDNKMGREVYGDDDTIEHF
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TLVQKHGFDISTULLBEDELBPETLEYHTIOAYTNNKTGKALKVDTFPHIELKVCD
LLATIAGFPERRFFELRQTGKKADP IGTDEVPKANTELVPVDHESSSMFRGLRDYRPIEN
NICHLINVSDGASNSLYGVGFGPLILTNRHLFERNNGELLIKSRHGEFVIRNTTQLQL
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LNMKSAVGALYKGKKKDYFAEFTPEMKEEILKQSCERLFLGKMGVWNGSLKAELRPLE
KVEANKTRTFTAAPLDTLLGGKVCVDDFNNQFYDHNLSAPWSVGMTKFYCGWNRLLES
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LDVTECGEVAALMCLAMFPCGKITCPDCVTDSELVQGQASAPNIKQRLAQLREVIKSS
YPRFKHAVQILDRYEQSLNGENANYQDFAEIQSLTDGMEKAAFPHANKLNAILIKGAT
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WMYEQLTGNLKAIAHCPSQLVTKHTVKGKCQMFDLYLKLHDGAREYFQPMLGQYQKSR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (11-OCT-2002) Kazusato Ohshima, Saga University, Faculty
of Agriculture, Laboratory of Plant Virology; 1 Honjo-machi, Saga,
Saga 840-8502, Japan (E-mail:ohshimak@cc.saga-u.ac.jp,
Tel:81-952-28-8730, Fax:81-952-28-8709)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /organism="Turnip mosaic virus"
/mol type="genomic RNA"
/isolate="IS1"
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PERI VSI LEWDRSKEPCHRLEAI CAAMI ESWGYDKL THEI RKFYAWV I EQA PFNSLAQ
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AATUCAAAACAACUAAGUUGAUUAGCGACUUAU 7477 |-:-|||| |-:-|||:-|| :-|| :-|| TATTCAAAGTGAGTAAGTTAATATCAGATCTTG 7148 SGANDACAUAGUUDAAUGAGUCAUAAGUACGAUC 7297 || : || || : | SGATTGCACAGTCTATCTAATTTCCAAAACTCCA 6968 7597 incegucaaucaaumencucungunggaaauacgu 7117 IUUUCUGAGACAAGCAAACAUUCCCACGAGUUG 7177 GCAAUCAAGUUAGAUGGUUAUAUAAUCAGCUUG 7537 -CCAACAAAACCGATGGATGTATGAGCAACTCA 7205 GTCCTAGTCAGCTCGTAACGAAGCATACAGTTA 7265 AUCUGCAAACUCGUAGUGAAGCGAAUGAGUUCU 7657 AGAGCGGUCUCAACAAGGAAGCAUAACAUUAAGG 7717 CAAUUGGGGAGGUCGACACUGAGAGAUUUGAAG 7777 UGAUGCAAUGGAACUUVAGGGAAUGCAAGUAUA 7837 : | : | :| || :|: TATGGAGCTATGGGTTCGAAACATGTAATTATG 7505 AAAAUUCCACAUTUGAUGAUCGAAAUCAUTUGC 7957 AAGGGGAAUUUGGGAAUUGGAAGGCUUUA 8017 ||| | :|||| ::|||| | :| |TGGGAAAAATGGGAGTTTGGAATGGATCACTCA 7685 UUCCCAAUAACUUUGUUACAAAGCACAUUGUGA CGUUUGAAGGCGAUUAUAUUAACAAGUUGAAGG

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Rajamaeki,M., Merits,A., Rabenstein,F., Andrejeva,J., Paulin,L.,
Kekarainen,T., Kreuze,J.F., Forster,R.L.S. and Valkonen,J.P.T.
Biological, serological and molecular differences among isolates of
Viruses; ssRNA positive-strand viruses,
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                                              CTCCCATATCAACACCCAGATGGCACACTTGTAAAGAAGTTCAAGGGGAATAACAGCGGAC
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CUCCAAUUGAAACUUUACUUGGCGGAAAGGUUUGCGUCGAUGAUUUCAACAACCAAUUUU
           AUGAUCUUCUAGGUAAACUUCCUGAUGGUUGGAUAUACCGCGAUGCUGACGAUCACGAU
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9337 9397 9041 9457 9517 9577 9637 9817 9877 8981 9101 9161 9221 2696 9757 9401 9461 9521 VRL 15-OCT-1999 Potato virus A RNA complete genome, isolate Her.
AJ131400
6K1 protein; coat protein; cylindrical inclusion protein; genome linked viral protein; component protein protein; palper component protein.
NID replicase; Pl protein; P3 protein; polyprotein.
Potato virus A Potato virus A Viruson. DNA stage; Potyviridae; CACAGAAGCAGTTTAACACATGGTTCGAGGGTGTCATGGCCGATTATGAATTAACGGAGG TOGCTGAAGCGTACATTGAAAAGCGTAACCAAGACGACCATACATGCCACGATATGGTC GUAUTUCACAGUUUAAUACAUGGUACAACGCUGUGAAGGAAUCCUAUGGUGUGUCUGAUG CAAACAUUAAUGGCAUGUGGUUUAUGAUGCAAGGGGAAGAACAAAUCGAAUACCCCCUUC UUGCUGAAGCAUACAUCGAAAAAGAGAAAUUAUGAGAAAGCCAUAUAUGCCGAGGUACGGUA GTGGCGCAAATAATAATTGTTCGGATTGGATGGTAACGTCGGCACAAGGTAGGAAGA CAAACAACGAAAAAAGACAAGGAUGUCGAUGUAGGAUCAAGUGGAUCUUUCAUCAUACCAC ------GAACGAGACAGAGAGTCAATGCTGGAACTTCTGGAACCTTCAGTGTGCCTA GAAUUAAAUCGAUAUCCAAUAAACUCACAAUGCCAAAAGUGAAAGGGAAAGGAAUUUUAA AUTUGGAGUUCCUUTUACAAUACACACCAGAUCAAGUGGACAUTUCAAAUACCAGGGCAA accricáricaciridaricarácciccicadacaaaccicarinarcacacaricaa **AAGAAAUGGGAAUAAUUUUGAAUGGAUUAAUGGUUUGGUGUAUUGAAAAUGGAACAUCUC** AACCAAUAGUGGAAAAACCCAACUTUGCGUCAGAUUAUGGCUCACUUUAGCAAUG UUCAACGGAACCUCACCGACAUGAGUUUGGCGCGAUAUGCUUUUGAUUUCUAUGAAAUGA CAUCAAGGACGCCAGCUCGGGCCCGGGAAGCCCACAUCAGAUGAAAGCUGCAGCAUUGC crrrragaacrccaaracereceaeaeaeaeacacacarccaeareaaaecaecaecaerec GAGAUGCGAAUAAUAAGAUGUUUGGACUGGAUGGAAAAGUCGGAAAUGCGACUGAGAACA CGGAGCGCCACACCGCAGACGAUGUUAACCAUAACACUCAUGCAUUCACGGCGUUCGAU 9522 CGGAGAGGCATACGACCGAGGACGTTAATCGGAACATGCACACCACCTACTTGGCGTTAAGG 9938 AUUAUUAGAUAUUUVACCUAAGCAUAGUUUUAUCUAGUAUCUUU 9980 GGATGTGAAGTTGTATGATAGACTATAAATAAAGTTT 9624

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Direct Submission
Submitted (16-DEC-1998) Kekarainen T., Dept. Plant Biology, Swedish
University of Agricultural Sciences (SLU), P.O.Box 7080, Uppsala,
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BEPTRELAENVTKQLKSDPFHVSPTLRNRGAVFGSTPIHVNTTGFALHYLANNLKNLL
TYDFI IDEFHVHDSNAIALAFHNYGGKLIKVSATPPGREVEFSTHYPVEIRVE
DOVSFQDPVKAQCGSNLDLFSRCDNLLVYYASYNEVDQLSKLLLEHFLYTKVDGR
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KVSISYGERITRGLSVGRARMGAVALRIGHTEKGISDVPVVIATQAPFLCFVGLDSTI
OSVTYOVLSNYTLKORARMGAVALRIGHTEKGISDVPVVIATQAPFLCFVGLDSEIO
LSKLAIPSKCYPIWMTGKAYRLLTHNSQIPDHVRVPFLTKEIPDKLHENVWAIVEKFK
GOBGIGRATSAQASKVAYTLETDIHATORTILIDQLLERENDKOGSGFFEWTNQSCSS
GMLSLCTTWANAIQSYR XRNTFRGIEIL ORDILLINGSESTLEFSTLE
AVORGSGTOVSNFLGLEGHWKKSLITKDLIVGGCVCVGAAMMIGEYFFKKSKEVVAFQ
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SQPIDKYFRAPRONAPKREILKYVGFTQSPYTHYQELMBILVLGGRAFPEQLG
SASAHLLETTRRVRNRTUNIKKGSLALFRNKISAKAHVNTALMCDNQLDRNGNLIWGE
RGYHAKRFFSNYFDIITPGVGYKQYIERRVPNGIRKLAIGNLIVTTNLEALREQLEGE
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LPTDISTQMYIAKSGYCYINIFLAMLVNVDESDAKDFTKKVRDIIVPDLGEWPTLIDV
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FVNMYGFDPSDYTFIRYVDPLTGYTLDESPYTDIRLIQSQFSDIREQQLLNDELERNM
VYHRPGVQGYLVKDKTSQILKIDLTPHIPLKVCDATNNIAGHPDREGELRQTGKGQLL
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NQHLEVRNNGSLTVRSQMGVFKVNSTVTLQMRPVEGRDVLIIKMPKOPPPFPQRLKFR
OPTHSEKVCLIILTNFQQKSSSWVSTSHIIPKENTYFWKHWISTKGGHCGSPIVSTT
DGAILGAIHSLSNMTYENYFACFPKGFTETYLATESAHEWVKGWKFNASNVCWGSFHL
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VTSIIFAGTTPPSMIETETIVKKIHTVGKHAKVMRKRSYITPPTDKSLHHHGVTPYSV
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VDTSTTTIMQTLFLKTARTNANLDVLTHGSSGLVFWNYLVTGQRMRTRDNFII VRGRC
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ESALTGLLHNLGRWGFTTACYTTDEDSIYAALNMKAAVGALYRGKKRDYFDAMSPSER
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LRIRLHFMEDWDIGSQMLQNLYTEIGTHQSQHQMAQLLKKFKGNNSGQPSTVVDNTLL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    translation="MATQAIMVGEFKILEVNCKPHAPVAAIHVPTQTPKTNDIQWADI
                                                                                                                                   Valkonen, J.P.T.
Comparison of the complete sequences of five different isolates of
                                                                                                   Kekarainen,T., Merits,A., Oruetxebarria,I., Rajamaeki,M. and
Valkonen,J.P.T.
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/db_xref="Gi.6066611"
/db_xref="GOA:090BT7"
potato A potyvirus
Phytopathology 88, 311-321 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     organism="Potato virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /mol_type="genomic RNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         db_xref="taxon:12215"
                                                                                                                                                                                                       potato A potyvirus (PVA)
Arch. Virol. 144, 1-12 (1999)
3 (bases 1 to 9587)
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                                                                   REFERENCE
AUTHORS
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AUTHORS
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KYSIQFDEQMEEEDDMYYFQAGTLDAGETPAQKSEGKKKEGEGNSGKAVAVKDRDVDL
QTAGTHSVPRLKSMTSKLTLPMLKGKSVVNLDHLLSYKPKOVDLSNARATHBQPQNWY
DGVKASYELEESSMEIILLORPWWCIENGTSPDINGVWTWMDDEEQVSYPLKPMLDHA
KPSLRQIMRHFSALAEAYIENGRSREKPYMPRYGLQRNLRDGSLARXAFDPYEITATTP
VRAKEAHLQMKAAALKNSNTNMFGLDGNVTTSEEDTERHTATDVNRNMHHLLGVKGV"
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                    EFNSRSKDKKDLWFMSHKAIQCGEILIPKLEEERIVSILEWDRSHEPIHRLEAICASM
VESWGYPELTHEIRRFYAWVLEQSPYNALATTCLAPCIAESALKTLYTNVHPTSTELE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   963 AATTTCATTATAGTGAGGGTAGATGCAATGGTGTATTGGTGGATGCCAGAGCAAACTA 1022
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   1783 GAGGAACUUGAAUCUUUCAGGCGUAAAAGGAGCCAAUUGGCAAGUAAAUUAUCCAGUCUU 1842
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1663 GCCACUAVAAACGUUGAGGAGUGUGGCGAAAUGGCAGCCAUUGUAAACCAACUCCUAUUU
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                                                                                                                                                                                                                                                                                                                                                      /product="cylindrical inclusion protein" 5529. .5687
                                                                                                                                                                                      product="P1 protein"
1053. .2426
product="helper component proteinase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="genome linked viral protein"
6256. .6983
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/product="NIa proteinase"
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8532. .9338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /product="coat protein"
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3624. .5528
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6984. .8531
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AAAUGCGGAUUCCAAGAGUUCGGAGCUUUAGAA 6039 | : | | | : : | | | | 3 3AGTCAGCATTGCGTGAATTTGGGTACTTAGAG 5513 UUUCGGGAUGCUCGCGAUAAGAAAAUGGGUCGA 6270 5033 5739 UCAAUUGGAAAACUCUCGGAUAUAUUGACGCC 5799
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TCTATCCAAAGAACTATTCTCATTGATGAA 5273 5859 UUGCAGGCAGCAAAGAAUCAAAUACUGGAAUUC 5979 AUUUCAAAAUUUCUAAAUCUGAGGUAAGUGG 6099 UNAGUUUGUUNAGGUGUCACUAUUGGUGGUUUC 6159 :: : : : || |: ::||:|
rrgatagtrggggagtgrrgrrggrgggggg 5633 AACAUUGAAGAAG------UUCAUCAUGAA 6210 AUGGGCGAAAAUCAAGACGUUUCGUUAGUAUG 6390 AGTGTTACAACACAAGTTTTATCAAATGTAACA 4853 unidadiugococcunacumangocumoacum 5439 SAAAUUCACAAGCAUUUAAUUCCUUACAAGUUA 5499 | |::||||| | : | :||||| :| 3CCATTCACAATGAACTCAAGAAGTACAAACTA 4973 AUGGCUUTUDACUTUDACCGUAACAUCUAUTUGG 5559 3GAAUCCAUCUUGAUUUACCGCGCGAAGCAAAA 5619 ACTCATAACAGCCAAATTCCGGATCATGTCAGA 5093 SAUAUGAAAUACCGACACUUGUGGGAAGAUAUU 5679 AUAGCAAAUGCAAUACGGAACCACUAUGCUAAG 5919 |:||| ||||| ||||| Arggaaccacaggttcgtgaatatg 5873 UUUAUUAGAUACAUAGAUCCCAUAACUGGAGCA 6450 SGUAGAAUGAGUGUUGUUAGCGCAACAAAGUA CAUCAUTUDAAAGCAAUGACAAGUAACGCAUGU : ||: :| CTTGCTATTCCTAGCAATGCGTCCCTATCTGG

7531 7011 7071 7651	Oy 7711 AUDAAGGACCUAUUU Db 7191 ACAGGATCTCATG OY 7771 UUUGAAGAUCAGUC Db 7251 TTTCAGAGTCTCTG OY 7831 AAGUAUAUCACCGAU Db 7831 AAGUAUAUCACCGAU Db 7311 TGTTACACCCCAT	Oy 7891 GCGUUGUACAGUGGUI Db 7371 GCATTGTATACAGGGI OY 7951 CAUUUGCUACAGCUU OY 7951 CAUUUGCUACAGCUU OY 8011 AGUCUUAAAGCUGAA OY 8011 AGUCUUAAAGCUGAA OD 7491 TCTCTCAAAGCAGAG	Oy 8071 ACAGCAGCUCCAAUUU Db 7551 ACAGCTGCACCAAUUU Qy 8131 CAAUUUUAUGAUCUUU Oy 8191 GCAUUGAGAAUCAUU Oy 8191 GCAUGGAAUCACUU Oy 8251 UCACGAUUUGACACUU Db 7731 TCGCAGTTTCACTTC Oy 8251 UCACGAUUUGACGU	
6451 ACGCGUGAUGAGAGUCCUUUGACAGAUGUGGAAUUAGUGCAAGCUCAUUUCGGAGAAAUC 6510	5=5 8 8 4=3	GUAGCCAGCGCUAUUGCCAACUCACAACAAUGGUCGGUCCACCACAACUUAU IIIIIIIIIIIIIIIIIIIIIII		6654 AAGGAAAACACATACTTTTGGAAAAGATAGGACAAAAGAAGGAGCACTGTGGATCT 6713 7231 CCUUMAGUUAGUUACUCACUGAUGAAUUUAUUGUAAGAAUACAUAGUUUAAUGAGUCAUAAG 6714 CCAATAGTGAGCACAACAGATGGAGTTCTTGGGAATACATAGTCTATCCAACATGACA 6773 7291 UACGAUCAUAAUUAUUCUCGAACUUUCAACGATAGTTTTCCCAACATGACAAGGATTCACAGAAACATTTTTTTT
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7650 7710 7590 7070 7190 7890 7370 7950 7430 8010 7490 8070 7550 8130 7610 8190 7670 8250 7730 8310 7790 8370 8429 7909 8489 7969 8549 8029 7130 UAAAUACUCAUCAGAAAUACCAAUUGGGGAGGUCGACACUGAGAGA 7770 UGGGCAAGUCAUCGAAAUUAUGAUGCAAUGGAACUUUAGGGAAUGC 7830 ::||||||: || ||||:||: | |||:::| ||||| |||: TTGGGACATTGGATCTCAGATGCTACAGAATTTGTACACAGAAAT- 7849 JAUUGCUUGCAAUCAAUCCAAAAUUUAUACACAUCCUAGAUUCUUU 8609 UUGUGACCAGAUCUUUGAAUCAUUGAACAUGAAAGCGGCAGUCGGU JGCAACACCUGAUGGAACAGUCG-UCAAAAAGUUUCGAGGAAAUAA CTCAACACCAGATGGCACAGTTGTTAAAAAAGTTCAAAGAAATAA :| : ::||||: | ||| | : :: IACTAATTGCAATTAGGCCAGATATGGAGCATAAGCTAGATGGATT UUUGAAAGCGGUUGCAACUAUUCCCAAUAACUUUGUUACAAAGCAC CATCCAGGCAGTGGCACAACTAGAAAGCAATCTGGTCACAAAGCAC AUGUAAAUUGUUUGAAUUGUAUCUGCAAACUCGUAGUGAAGCGAAU ACUGAUGGGUUUCUAUGGGAAGAGCGGUCUCAACAAGGAAGCAUAC | : : | | : : | 3acregactreaterece UAAGAAAAAGGCGUACUUCGAAAAUUCCACAUUUGAUGAUCGAAAU saadaadceceattactttgaceceatgacececagtgacadaaa JUCUCUTACACCAUACUTGCTGGAATGCAGTGCTCCGGGATTTAGGGGAG JUGGGACAUAGGCGUGCAGAUGCUUCGAAAUUUGCACACUGAAAUA AUAGUGUAAAGUUUGAGAAUCAGGAUGAUGUCUGCAGGUAUUUCGU JGAAACUUUACUUGGCGGAAAGGUUUGCGUCGAUGAUUUCAACAAC JAAUAUGAAAUGCCCAUGGACAGUCGGGAUGACUAAGUUUUAUUGC : AACAGUCGUAGAUAACACAUUGAUGGUCUGUAUUUGUGUGCAGUA

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Production of strain specific antibodies against a synthetic polypeptide corresponding to the N-terminal region of the plum pox
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Forestali, Dip di Biologia, Via Nazario Sauro 85, 85100 Potenza,
ITALY. NEW ADDRESS (18-DEC-2003) Dipartimento di Biologia, Difesa e
Biotecnologie Agro-Forestali, Universita degli Studi della
Basilicata, Viale dell'Ateneo Lucano n. 10, Campus Macchia Romana
3A310, I-88100 Potenza, ITALY
On Dec 19, 2003 this sequence version replaced gi:2960346.
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Submitted (04-DEC-1996) A. Crescenzi, Difesa e Biotecnologie Agro
Submitted (04-DEC-1996) A. Crescenzi, Difesa e Biotecnologie Agro
Forestali, Dip. di Biologia, Via Nazario Sauro 85, 81100 Potenza,
ITALY. NEW ADDRESS (18-DEC-2003) Dipartimento di Biologia, Difesa e
Biotecnologie Agro-Forestali, Universita degli Studi della
Basilicata, Viale dell'Ateneo Lucano n. 10, Campus Macchia Romana
3A310, I-88100 Potenza, ITALY
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                                                                  9086 GTATGGTCTTCAACGCAACCTGAGAGATCAAAGTTTGGCAAGGTATGCATTTGATTTTTA
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J. Virol. Methods 69 (1-2), 181-189 (1997)
98163291
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/mol type="genomic RNA"
/strain="Sweet Cherry"
/db_xref="taxon:12211"
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                                                                  AGGAGAACUUUGGUUUAUGUCUCACAAAGGAGUUAAAUUAAAUGACAUGUAUAUUCCAAA
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RLLKSYRLRDSEVI LNKLAI PNGNVGGWMSVRDYKRQGCNLDLDDNVR I PFYVKDLPE
LLHEQIWQAVERYKSDAGFGRICSSARKIAYTLQTDIHSI IPRTVKI I DVLLEGERTK
CAHFRAWTSQSCSSSNFSLSSI TSAIRSKYAKDHTEEDIGULQMAKAQLLEFQNLNI I
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RNEQIGDDKI TPQHIRANPGILVAYYKDATOKALK I DLITPHHPLRVCDKTATIAGFPB
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GARNSEMFGLGPGGVI I TNQHLFKRNDGELTI RSHHGEFVNDTKTLKLLPCKGRDI
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KGGMMTVQDYSEASDRLRELARYQKNRTENIQSGSIKAPRNKISAKAHVNMQLMCDNO
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GLKPRYDI TLDEATKKI VQI FANTSGFKHVHGKGEI TPGMSGFVI NPRNI SDPMQI HD
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RRTAKSLINTYESATASAWKGLEEKLQPWFAKREFSKTITKRKGLRCFKASSEQVIER
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protein_id="CAF02291.1"
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/product="6K1 protein"
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5556. .5714
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/product="HC protein"
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clone="PPV-SwC 3"
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| AATTITCACATGTGCTTTGCGTTCCTCAAGAGATATCGTGAATTAATGCGGGTTGAGAATC 1401
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1702 AAAGGGAGTATCATGCCAAGCGCTTCTTCGGAACTATTCAATGTGATAGACACAGTG
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                                                                  /product="replicase"
8580. .9575
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:	2330 GAAAACUGAUUUUAUCGACGAUCCAUCUACGCUACGACAAACAA	2390 UCACAAGAGUUCCAGUUGGUAAAUAUUGUACAAAGCAAAAGAGAUGGUUGUUACGUCUAUC	1882	1942 ATGTTGCTGTTACACACGACGCACACCATTGGAATCTGAGATCATAGCCCAA 2001	2510 CUAAGAAUCAUCUAGUCAUUGGAAAUUCAGGAGAUCCAAAGUAUGGAUGUACCAAGGA 2569 	2570 GCUCAAGUGACAUGUGGCUAAGGUAAGGUUAUUGUUAUCUCAACAUUUUCUUGG 2626 	2627 CAAUGUUGCUGAAUGAGAAUGAGAGUGAAUCCAAAAAUCAUCACAAAGAAGGUUAGAGAUA 2686	2687 UAAUUGUACCGCGUCUCGGUCAAUGGCCAAGCUUAAUCGAUGUUGCAACUGAAUGUUACU	2182	2242 TTCTTGCAGTGCTATATCCGGAGACTCGAACGCTGAACTCCCAAGGATACTTGTTGATGATC	2807 AUACAUCAAAAUGUAUGCAUGUGAUCGAUUCAUAUGGCUCGCUAGACACGCAAUUUCAUG 2866 2302 ACGAATCAAAGATATTTCATGTCGTTGATTCGTATGGTTCATTATCATGACGGCCATGCAC	2867 UUCUGAAGGCAAAUACUGUAAGUCAGCUAAUUAAAUUCGCCGAUAAUGACUUGGAUUCGG	2362 TCCTGAAAGCAACACAGAACCAACTTATAAGCTTTGCAAGTGATACGCTAGACTCAA 2421	2927 AGCUGAAACAUUAUUUAGUAGGUGGAGACCUCCAUAGCAAGCUCCUCAGUGUUCCA 2986 : : : : 2422 GCATGAAAATGTATCCTTGGAGGTCTAGAGGTTGATCGATGCGATGAATTCAAGAATG 2481	2987 UAAAAUUACUCUGUAAAUGUAUAUAUAUAGGCCUAAAUUGAUGAGCAAUGCAUUGAGGAAG	2482 TGAAACTCCTCATCCGGAGTATTTATAGACCAGAGTTAATGCAACAAGTGCTGAAG	3047 AGCCUUDUUGUUGAUUAAUUAAGGGGGGGACACCAGAGAGUUAAUUAA	3107 GUCAGCAUUUAGAAUUAGCUUUAAAGUACUGGAUGAGCAACAACAGUCUGUCGCUU 3166 	2602	3167 UAUUUGCAAUGAUCCAUGGACUAGCUGCAAAAGUAACAGUUGCUCAAACAUUGAAUGAA	3227 AGAGACUAAUACUUGAACGCGGGGGGGGGGAAUUUGAUUUCGGUCAUGGAAACCAUACACA 3286	2722 AGATGAATGTTATAGATGAGCATGCATCAGTCCTCTATGATAGTGTTTTCAACGGGACAA 2781		3347 ACAUGAAUUCCACUCUUGAUCUCGCCGGAUUCAGCAUAUUACAAUCAAGAAGUAGUAUGU 34
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3676 IGGATGAGAAGAAAGATTAATTTTTGTTTTTGCAAAGTAATGAGGTTGCACCAACAG 3735 3315 3435 3915 3826 3887 UCAAUCCAG-----ACCUGACAAAGGAAGAAUUUAAGGAGUACAUUGCAAGAAGAAGAGAC 3940 4235 AGUUCAAGGAGAUGAACUUUGCCGCAUGGUGGGAAAAAAACAACUACAAUGUGAUAGAGUGG 4294 3736 TICCITITGACICCAACATICGAAAGIGGIGGACGAATCCAAACTCGAAATGICA 3795 4355 UGAGUAACACAAUAUCUCAUGCCCCUGAGAAAGAAUGGAUAGUCCGUGGUGGUGGUUGGAU 4414 4415 CAGGAAAAUCUACUGGUCUACCAUUCGCGUUAUCUAGUAAAAGGCGCAGUUCUUAUGCUCG 4474 3916 CAGGCAAATCTACTGGGCTACCATTTCACTTGAGCAAAAAGGGTCATGTCCTCTTACTTG 3975 3827 UGAAUAUCGAGAAAGUUCUGAUGAAUAAUUUAGUGGCCCUUCAUAAGGAGCAGCAGAUAAAGA 3886 UGAUUUUUGACUCAGAGAAAAGUGAUUGUGUAUAUAAAACACACUGAACAAAUUGCGAAAUC 4114 2842 AATCAGATCACACTGCATGACTTGGGCTTCTCCGTGTTACGGAATGCA---ACACCCC 2898 3467 UGGAAAAMUUACAAGAAAUGUGGCGAUUAUCAAAGUACUCAAUAUCUGGGAUAAGUCAAC 3526 3527 UUUCAAUGAAAGGCGCUACCGAUUUAGGCGGUCGAUAUUCAGUAUCUGCAAAGCAGUUUA 3586 3079 TTGGCAGCCAGTACAAAGGCCTGAAAGGGGAAATAAGACGAAGGAAAGACAGCGTAGTAT 3138 3941 CUGAGCUGAUUGCAUUAGUUAAUAAAGAAUUGCAAGAAGAA-----GUUGAUCAUCAAG 3994 3995 CUAAGCGCAAAGGUGAACAAAACUUGGAGAAAAUUAUAGCAUUUGUUGCCUUAGUUAUGA 4054 4295 UACCCCAUUAUAGAACCACUGGGAAAUTUAUUGAAUUCACUCGUGAAAGCCUGUGUAGUG 4354 3139 GTTATGCACCAGTCAATGGGGAAGCTATTCTGCAAAGCTGTCGTCTTTCAACGAATT 3259 TCGGTGCCACATGCAAATCCAT---GATCAATGAGCATCAGCTGCAAACAGATGGCTG 3407 AUUGGAUGGAAAAAAGUUAUCUCAUGGAAUUAGAGGAUUCGUGGAACGACUUAAAGUGGU 3587 UAACAUCAGUGAUGAAACCUGUCAAGAAAUCUUGUGUAAAAGCAAGAGAUACUUGUAAAG 3647 AAGUAAUCAUCAAUACAACAUCCUGGACAUUUCGGGCAACAUUUUCUUUGUGUAGGUGGU 3767 UNIGGCAUUCAGCUAAUUCUAUAUCGUUCGACUAUGCACAAAUGAAGAGAGAAAAGCAGG 4055

	5555 UUUGGCUAGAUUGUAAAUUUAUGACAGUAUAGGAAUCCA -	5615 CAAAAAUUCCAUUCCAUUGUAGAGAAUUCCCAGAUAUGAA :: ::			5735 AAGUAOCAUAUACACUUAAACAGACAUUCAUUCAUUGAUUGG [: : : : : : : : : : : :	5795 ACGCCUCUUGCAAGAAGAAUAUAGAAAACAGCAUUU	5239 A1G11GGPARCAGGGGACGCGACGARGCAGGCGADACGGCADA111		5915 CUAAGGACUACACUGCUGGCAAWAUUCAGAAAUUGCAGGC 	5975 AAUUCGUCAAUUUAAAUCUUGAUCCUUCGGCGAAAUGCGG ::	6035 UAGAACUAGUVACCÇAVÇAGAGGAAGAAAUVUÇAAA	: :::	6095 AGUGGAAUAAGUCACUAAUUACACGUGAUAUCUUAGUUUU 	6155 GUUUCUGGAUGAUAUGGGAUAAGUUCAAAUCAAACAUUGA	: : : : :	6215 AGAGGAAGACUCAAAAGCUUAAAUUUCGGGA 	6266 GUÇGAÇAAGUAUAGAÇAACQACGGUAÇUAUUGAACAUUA	5776 CCCGAGAAGTGTATGGAGATGATTCCACGATGGAAGAATA	6326 AGAGAGGUGCAGUUAAGGCCAGAAGAGAGAGAAUGGGCGA	6386 GUAUGUAUGGAGUUAAUTUAGAAGAUUTUGCUUTUAUDA	: : : see atatgtatacgatcctacagactacaactttgttcg	6446 GAGCAACGCGUGAUGAGAGUCCUUUGACAGAUGUGGAAUU 	6506 AAAUCAGAGACAAAAUGCUAGACGAGGCCUCAUCGAUAG	6016 TAATTCGAAATGAGCAAATTGGAGATGACAAGATĆACCC	6566 CAGGUUGACAGCANKOUAGUAAGGACGGGGUUAAUGC 	6626 AACCACACAAUCCUCUACUCAUAUGCAAAAACAAAGCGAC
-	OY 4475 AACCAAGACCAUUGGCAGAGAAUGUCUCACGACAGUUGAGACAACAUCCUUUUAUG 4534		4095		4655 AAUUUGUGAUAAUAGAUGACGUCCAGGUCCUAGAUAGCAACGCUAUGGCAUUCGUGUGUC 4714	UUCUCAAGAAGAACAAAUUGGAAGUAUUGAAAGUGUCAACAACAAGGGGGGGCC	TGTTATCGGAATACTCCTATCCAGGGAAATTCTGAAAGTCTCAGCGACACCTCTGGGC 4275	4775 GOGGALOGGARAUCCARACAGAGAGAGAGAGAACAACAAGAACAACAACAAGAGAACAAC	4835 UCCAAGCUUUUGUGAAGCUCAAGGAACUGGGUCUGCACGAGAUGUAAUCAAUAAGGGAG 4894		4455	4955 GAGANAAAGCGAUUUAGGGGGGAGGAGGGGGGGGGGGGGG		4575	5075 AGAAUGGAGUCACUCUAGAUGUAGAUGUUGUGGACUUUGGAUGUGAAAGUCACUGCUG 5134		4695	5195 GCANACAAAGAUUGGGCAGGGUUGGUAAGAAAAAAAGGGCAUGCAAUGAGAAUUGGAA 5254 4696 GGATTCAGCGACTCGGTGTTGGTCGAAACAAACAAACAAGCAGCAGCAGTTGGCGAATTGGTGATTGGTCGAAACAAAC		TCACAGAAAAAGGTTTAACACAGATTCCACCAATGATTGCAACTGAGGCCGCTTTCTTGT 4815	5315 GCUUCACAUUGABUUGCCUGUAAUGACACAAGGAGUUUCAGUUAACAGUUUUUCAAAUU 5374		4876 GCACGGTGAAGCAGGCACGAACTATGCAGCAGTTCGAACTGTCCCCTTTCTACACAGCAG 4935 S435 CACUUGUAUAUCAUGACAGGAUGCACCCUGAAAUUCACAAGCAUUUAAUUCCUUACA 5494	4995		4996 GGCTGCGGGACTCAGAAGTTGAATAAGTTGGCCATACCAAATGGCAATGTTGGTG 5055
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TTGCATGAACAGATATGGCAAG 5175 |: |: |: :|| || ATTTGTAGCTCTAGTGCTTGCA 5235 GGAAAAACUCUCGGAUAUAUUG 5794 AAUGCAĄUACGGAACCĄCUĄUG 5914 TCAGCCATTCGATCGAAGTACG 5415 ATGCCAAGGCGCAACTCTTAG 5475 SGAUUCCAAGAGUUCGGAGCUU 6034 : | | : | || CTTGTGCAC 5535 :| : || |: : :||:|
ATGCTTGGGGTGCTTGGTGGTG 5655 BAAGAAGUUCAUCAUGAAGGAA 6214 ||||||| | AAAGAAGATGCTCACCAAG 5715 | ||:|||||:|| caagctcgcgataaccggatgg 5775 JACUTUGGAUCGCCAUACGUCA 6325 || | || || ::||: | ACCAAGACGAGAAGTTCGTGA 5895 AGAUACAUAGAUCCCAUAACUG 6445 JUNGUGCANGCUCAUTUCGGAG 6505 :: |:||| || ::| TTGGTGCAGCAACACTTCTCTA 6015 AGGCAACACUUUAAAUAAAC 6565 JCCAUCAUGAAAGUAGAUUUGC 6625 : || : ||: AAGGCTCTCAAGATTGATCTTA 6135 AUGAGUGUUGUUAGCGCAACAA 5734 3CAGCAAAGAAUCAAAUACUGG 5974 meguadencacuamegue 6154 SAUGCUCGCGAUAAGAAAUGG 6265 SAAAAAUCAAGACGUUUCGUUA 6385 CAAAGCGACAAUAGCAGGUUUCCUGAGA 6685

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à	9260 GAUCUTUCAUCAUACCACGAAUTAAAUCGAUAUCCAAUAAACUCACAAAAGUGA 9319	
qq	8893 GGACCTTCTCAGTACCTCGACTTAAGTCTATGACTTCGAAATTATCACTCCCGAAGGTGA 8952	
٥٨	9320 AAGGGAAAGGAAUUUJAAAUUUGGAGUUCCUUUJACAAUGAAGACAGAUCAAGUGGACA 9379	
qa	8953 AAGGGAAGGCCATCATGAACCTCAGTCATTTGGCTCATTATAATCCTGCACAAAATAAGT 9012	
ð i	UUUCAAAUACCAGGGCAAGUAUUUCACAGUUUAAUACAUGGUACAACGCUGUGAAGGAAU	
a è	9013 TATCAAACACGCGGGCTCCTCAATCTTGTTTCCAAACTTGGTATGAAGGAGTCAAGCGAG 9072 9440 CCTATGGTGTGTGTGAAGAAAAAATGGGAATDATTTTGAATGGATTTAATGGTTGTTGTA 9499	
5 A	ACTACGATGTTTCGGATGATGATGATGATATTTTGAATGGTTTGATGGTGCGA	
ò	9500 UUGAAAAUGGAACAUCUCCAAACAUUAAUGGCAUGGGUUUAUGAUGCAAGGGGAAGAAC 9559	
qq	9133 TTGAAAGTGGAACCTCTCCAAACATCAATGGGATGTGGGTTATGATGGATG	
ć	9560 AAAUCGAAUACCCCUUCAACCAAUAGUGGAAAACGCAAAACCCACUUUGCGUCAGAUUA 9619	
Dp	9193 AAGTGGAATATCCAATAAAGCCATTGTTGGATCATGCGAAACCCACTTTTAGACAAATTA 9252	
'n	UGGCUCACUUUAGCAAVGUUGCUGAAGCAUACAUCGAAAAGAGAAAUUAUGAGAAGCGU - : :	
q	9253 TGGCACATTTCAGTAACGTCGCTGAAGCGTATATTGAAAAGCGGAACTATGAGAAAGCAT 9312	
දු සි	9680 AUAUGCCGAGGUACGGUAUCAACGGAACCUCACCGACAUGAGUUGGCGCGAUAUGCUU 9739 - - -	
λ̈	9740 UUGAUUUÇUAUGAAAUGAÇAUCAAGGAÇGÇÇAGCUCGGGGAAGCCÇACAUÇÇAGA 9799	
අු	9373 TTGATTTCTACGAGATGACCTCGCACACGCCTGTGAGGGCTCGTGAGGGCACATATTCAAA 9432	
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Papaya leaf-distortion mosaic virus; PLDMV; infection; resistance; gene;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "Papaya leaf-distortion mosaic virus protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A full length genomic RNA of papaya leaf-malformation mosaic virus, useful for creating a papaya leaf-malformation mosaic virus-resistant plant, comprises a sequence where a uracil is replaced by a thymine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Papaya leaf-distortion mosaic virus genomic RNA SEQ ID NO:1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (DOKU-) DOKURITSU GYOSEI HOJIN KOKUSAI NORINSUIS
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CGCACAAACAAAUUGCACAAAUUAUUGGCAGUCGCAAAGAAUUCCGUUUUGAAAUUUGG 1981 Qy 3062 UUUUAGCGUGUUUCACCAGGUGUUUUAUUAGUAAGCCAUGUUUUAUUAGCAGUGUUUUAUUAGAAUUAGCAGUGUUUUAUUAGAAUUAGCAGAUUAGAAAU 3121 AGCAUCUGAAUGGAAAUGAGAAUUAGCGAAUAAACUUGUUAGGAAUUUCUAUGAAA 2041 Db 3062 UUUUAGCGGUGUUUUAUUAUUAUAUAUAAUAAUAAUAAUAAUAAUAA	2041 Qy 3122 2101 Db 3122 2101						1482 AAAUGUGGCGAUUAUCAAAGUACUCAAUAUCGGGAUAACUCACAUAUCGGGAUAAGUACUCGGGAUAAGUCAACUUCAAUGAAAGGCG 3541	CUGUG UCAUC					AUGUA	AGGUA AAAUA 	COUNTY OF THE PARTY OF THE PART	OY 4022 AGAAAAUUAUGGAUGCCUUAGUUACGUGAUGAUUUUGACUCAGAGAAAAGUGAUU CUGUA 3001 Db 4022 AGAAAAUUAUGGCAUUGUUGCCUUAGUUAGGUAUGUUGACUCAGAGAAAAGUGAUU CUGUA 3001 Db 4022 AGAAAAUUAUAGCAUUGGUUGCCUUAGUUAGGUAUGUUGACUCAGAGAAAAGUGAUU	Qy 4082 GUGUAUAUAAGACACAGAAAUGCCACAAAUGCCACAAGACACCGCGCACAACAGGACCACGCGAACAAAUGCGAAAUGCGAAAUGCGAAAUGCGAAAUGCGAAAUGCGAAAUGCAACAAGAACCGGAAAUGCAACAAGAACCGGAAAUGCAACAAAUGCAAAAUGAAAUGAACAAAAUGAAAUGAAAAUGAAAAUGAAAAUGAAAAUGAAAAUGAAAAUGAAAAUGAAAAUGAAAAUGAAAAUGAAAAUGAAAAUAGAAAAUAGAAAAUAGAAAAUAGAAAAUAGAAAAUAGAAAAUAAAAAUAAAAAA
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	RESULT 2 AAP26998 ID AAP26998 standard; DNA; 9760 BP. XX AC AAF26998; XX DT 10-APR-2001 (first entry) XX XX XX XX XX XX XX XX XX
	9122 AGAAUAAAGAAAAGAAAAAUAAAAACAAAAUAAAGAAAGA

Weakly toxic strain of Dioscoreaceae mosaic virus used in the genetic diagnosis of the mosaic virus infection and for the management of crops resistant to the virus.

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Claim 1; Page 6-20; 22pp; Japanese.

The present sequence encodes the Japanese yam mosaic virus (JYMV) JYMV-M protein sequence. JYMV is a weakly toxic strain of Dioscoreaceae mosaic virus having a modelic acid sequence which shows insorceaceae mosaic virus having a mucleic acid sequence which shows interference against the infection of a strongly toxic strain of Dioscoreaceae mosaic virus; (2) a Dioscoreaceae mosaic virus resistant crop which is a plant of Dioscorea alata and is infected artificially by a weakly toxic strain of Dioscoreaceae mosaic virus; (3) a method for the cultivation of a Dioscoreaceae mosaic virus; (3) a method for the cultivation of a Dioscoreaceae mosaic virus; (3) a method for the weakly toxic strain of Dioscoreaceae mosaic virus is infected to the weakly toxic strain of Dioscoreaceae mosaic virus is infected to the tubercle or the bulbin of a plant of Dioscorea japonica, Dioscorea opposita or Dioscoreaceae mosaic virus is which a DNA fragment and the tubercle or bulbin is grown; and (4) a method for genetic diagnosis of a Dioscoreaceae mosaic virus in which a DNA fragment amplified by using reverse transcriptase-polymerase chain reaction (RT-PR) Primers atagetteacacaccecteac (AAF32201) is treated with a restriction enzyme to distinguish the weakly toxic strain of Dioscoreaceae mosaic virus from the strongly toxic strain Dioscoreaceae mosaic virus

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Sequence 9760 BP; 3339 A; 1851 C; 2171 G; 2399 T; 0 U; 0 Other;

GGGCACAGUGGACAUAUCAUUCAAUAUGAUAAGUUUAGAGGUUUGAGUGGACGGCAUUUC 1479 1158 AATGGGTTCAACAC---AGCTTTTCAAAGATACAGGAAACAAGATCGTGAGCACACATGT 1215 GAAGAGGAACUUGAAUCUUUCAGGCGUAAAAGGAGCCAAUUGGCAAGUAAAUUAUCCAGU 1839 CUUCAUAUCAAAUUUCCUUACGUGGAUCAUUUUCUUAAUCGAUAUGAGAAUAGUCUGAAU 1899 CGGAUGAACACAAACUUCGAUGCGCACAAACAAAUUGCACAAAUUAUUGGCAGUCGCAAA 1959 GAGAUUCCUUUUUCAAAUUUAGAGCAUCUGAAUGAAUUGCUAAUUAAGUCGGAUAAACUU 2019 CTTCCTGCTTTTAGCCAGGCAAATGCCTAAATGATGATGTTCCTAATAAAAGGAGGTAGTGCA 1575 2020 GUUAGCGAGGAUTUCUAUGAAAUGUCUCAAUGCCUUUUAGAGCUAACACGCUGGCAUAAA 2079 | :||: ||: || : | | | CTCATTCAGATACTAGAAAGGCAAAGGCATTACAA Tratoccaaacaaracecaegaagaragrecearrigererearceaegeerraaarriree **AAAGGUUUUGAUCGUCAAUUUAUUGACAUUCGAGAUAGACCUAAGAACGCUCAUGAGUGC** GGAAGUUACAUCAUUGUUAGGGUUAGCAUGGAUGGCAGAAUUAUUGACGCUCGUUCAAAG AUCACACACCAGCGUUAUGAUCAACAUGACCCACUACAGUGAUGCAGGUUUGAGUUUUUGG UUUCCAAUGUGGAAAAUAACAUGCACUCAAUGUGGAGAACUGCUUGAAAUGUUGUCACAA CAAGCGACGCATGAAAACATACTCAAGAACAACAGGAAATACGTCACATCGTTCTTCAA **AAGGCCACUAUAAACGUUGAGGAGUGUGGCGAAAUGGCAGCCAUUGUAAACCAACUCCUA** | : | | | | | | | : | | AGTGTGAACAGCAATTATACAGAGATTCATAGTCTCTCAGAAGGGAAÃACA Length 9760; 23.3%; Score 2363.6; DB 5; 40.7%; Pred. No. 0; llarity 40.7%; Pred. No. 0;
Conservative 1339; Mismatches 3669; Best Local Similarity Matches 3517; Conser 1420 1039 1540 1159 1216 1276 1780 1336 1900 1480 1099 1600 1720 1840 Query Match 979 셤 ઠે g a g 요 요 ò ઠે 셤 ઠે ద ઠે ઠે ठे ò 윤 ठे ઠે

2475 1815 1935 2439 2499 2115 2616 2175 2676 2235 2415 2916 2535 AGGCCUAAAUUGAUGAGGCAAUGCAUUGAGGAAGAGCCUUUUUUUGUUGAUUUUAGCGUGU 3072 3073 AUCUCACCAGGUGUUUUAUUAGCUUUAUAUAUAGUCAGCAUUUAGAAUUAGCUUUAAAG 3132 GATCCAACAGAGTACCGAACACCATCTTGGCATCTAAGGAGACTCATAAAAGGCATCTAC AACAGGAGCGAUUCAUUCAAGAAGGGAGAGAUUCACCAUUUCCGAAAUAAGAUGUCAGGU GUGUGGGGUGAAAGAGGUUAUCAUGCGAAGAGGUUUUUUCUUAAACUUCUUUGAGAAAGUU 1816 GATCCTAGCAAAGGATATGCAAAATTTGAAGCACGTATAAACCCAAGGGGCCAAACGCAAA 1876 ACAGCAATAACCAGGCTAATCGTGCCAACAATTTTGAAGTATTGAGAACAGAACAA GGUAGCCCAAUCACAAGAGUUCCAGUUGGUAAAUAUUGUACAAGCAAAAGAGAUGGUUGU GGTGAATCAATTGGAGAACACCCATTGACTGTTGAGTGTACTAGTGTACTGAATGGTGAT AAGAUGCCAACUAAGAAUCAUCUAGUCAUUGGAAAUUCAGGAGAUCCAAAGUAUGUGGAU GUACCAAGCAGCUCAAGUGA - - CAUGAUUGUGGCUAAGGAAGGUUAUUGUUAUCUCAAC AUTUTUCUTGGCAAUGUTGCTGAAUGTGAATGAGAGTGAATCAAAAUCAAAAUCACAAAGAAG | : ::|::|||||:| : |||||| | ATCTTCTTGGCAATGCTAATGTTAATGTGAAAAAATG GUUAGAGAUAUAAUUGUACCGCGUCUCGGUCAAUGGCCAAGCUUAAUCGAUGUUGCAACU Greadadargrectraraarcagcreddeacardcectracactrredacgraddaagr GAAUGUUACUUCCUAUCAGCCUUCCACCCUGAAACGAAAAAUGCUGAGUUGCCCCGAAUU CUAGUGGAUCAUACAUCAAAAUGUAUGCAUGUGAUCGAUUCAUAUGGCUCGCUAGACACG CAAUTUCAUGUUCUGAAGGCAAAUACUGUAAGUCAGCUAAUTAAAUTUCGCCGAUAAUGAC --------CUCCUCAGUGUUCCAUAAAAUUACUCUGUAAAUGUAUAUAU 2440 UACGUCUAUCCAGCAUGCUGUGUUACAAUGGAAGAUGGUACGCCAUUGUUUUCUGAUAUC GGTTATCACATCCTAAAAGCGAACACTTGAACAATTAATCAAATTCACACGTGCAGGT GAUUCAACUGACGGUUAUAAGAAACACAUAAUGCGAGUCAACCCCAAAUGGCCACAAGACAA 1696 2500 2560 2176 2236 2200 1756 2260 2320 2380 2617 2677 2296 2797 2917 2972 2737

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4264 4741 5041 4624 5101 4684 5161 5281 4501 4084 4561 4621 4204 4681 4324 4801 4384 4861 4444 4921 4504 4981 4564 ACUUAGAUUGUGAGGGGA---GCAAAGUUACAGAGUUCAAGGAGAUGAACUUUGCCGCAU 4261 ACAAGGACATCATCTTAATGGGAGCAGTTGGATCTGGAAAATCAACAGGCTTACCATTTC AACTGTCCCAAGATGGTGTACGGACGCCTCCGAATGTCATGGAACACACTTTCAGTACGT UUAUUGAAUUCACUCGUGAAAGCUGUGUUAGUGUGAGUAACACAAAUAUCUCAUGCCCCUG CGUUAUCUAGUAAAGGCGCAGUUCUUAUGCUCGAACCAACAAGACCAUUGGCAGAGAAUG UCUCACGACAGUUGAGACAACAUCCCUUUUAUGCAAACCCCACAUUGAGAAUGCGAGGAA GAAAACATTTTGTCGTGGCAACGAACATCATCGAGAATGGAGTCACATTGGATATTGAAG UNGUUGUGGACUUUGGUUUGAAAGUCACUGCUGAAAUUGAUUACGACAACCGGUGCGUUA AUUACACAAAGACCCAUUUCAUACGGAGAACGCAUACAAAGAUUGGGCAGGGUUGGUA GGUGGGAAAAACAACUACAAUGUGAUAGAGUGGUACCCCAUUAUAGAACCACUGGGAAAU AGAAAGAAUGGAUAGUCCGUGGUGGUGGUUGGAUCAGGAAAAUCUACUGGUCUACCAUUCG UUGCAAAUAAUCCUCUAAAAUUAAGUGAUUUUGAAUUUGAAUUGAUGAUAAUAGAUGAGUGUGUCACG UCCUAGAUAGCAACGCUAUGGCAUUCGUGUCUUCUCAAAGAACACAACUAUGAUGGCA CAGUIUCCAUUCAUAUAGAGGAACAACUIVAGUUUCCAAGCUUUUUGUGAAGCUCAAGGAA CUGGGUCUGCACGAGAUGUAAUCAAUAAGGGAGACAACAUUUUAGUGUAUGUUGCUAGUU ACAAUGAGGUUGAUCAGCUCUCAAAAAUGCUCGGAGAUAAAGGCUAUUAGUGACUAAAG UCGAUGGCGUACCAUGAAAAUUGGUUCGACCGACAUAGUUACUAAAGGGAGUAGCCAGA AGAAACAUUUCAUUGUAGCAACCAACAUAAUCGAGAAUGGAGUCACUCUAGAUGUAGAUG 3845 4445 5162 4322 4382 4442 4205 4265 4325 4802 4862 4922 5042 4745 5222 3785 3905 4502 4085 4682 4742 4505 5102 4805 4982

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7520 GGUJAJAJJAAUCAGCUUGAAGGAAAUUUGAAAGCGGUUGCAACAUUUCCCAAUAACUUUG : : : :	rug 7579 : : :TcG 7201
7580 UJACAAAGCACAUUGUGAAAGGACGAUGUAAAUUGUUUGAAUUGUAUCUGCAAACUCGUA :: : - : - : - : - : - : - : - : - : - : -	GUA 7639 : :ATG 7261
7640 GUGAAGCGAAUGAGUUCUUUAAACCACUGAUGGGUUUCUAUGGGAAGGCGGUCUCAACA 	ACA 7699
7700 AGGAAGCAUACAUUAAGGACCUAUUUAAAUACUCAUCAGAAAUACCAAUUGGGGAGGUCG 	ucg 7759 :- rcc 7381
7760 ACACUGAGAGAUUUGAAGAUGCAGUUGGGCAAGUCAUCGAAAUUAUGAUGCAAUGGAACU 17160	ACU 7819 : :GGT 7441
7820 UVAGGGAAUGCAAGUAUAUCACCGAUUGUACCAGAUCUUUGAAUCAUUGAACAUGAAAG :: - - - - - - - - - - - - -	AAG 7879 -
7880 CGGCAGUCGGUGCGUUGUACAGUGGUAAGAAAAAGGCGUACUUCGAAAAUUCCACAUUUG 	пис 7939 .aag 7561
7940 AUGAUCGAAAUCAUUUGCUACAGCUUAGUUGUCUCCGAUUAUUCAAGGGUGAUUUGGGAA 	GAA 7999
8000 UUUGGAAUGGAAGUCUUAAAGCUGAAUUAAGACCAAUUGAAAGGUUGAAGCAAAGAA ::	AAA 8059 AAA 7681
8060 CGCGAACAUUCACAGCAGCUCCAAUUGAAACUUUACUUGGCGGAAAGGUUUGCGUCGAUG 161	AUG 8119 -: ATG 7741
8120 AUUUCAACAACCAAUUUUAUGAUCUUAAUAUGAAAUGCCCAUGGACAGUCGGAUGAUGAUA :::	CUA 8179
8180 AGUTUNAUVGCGGANGGAAUGANCCUUCUAGGUAAACUUCCUGAUGGUUGGAUAUACCGCG 	GCG 8239
8240 AUGCUGACGGAUCACGAUUUGACAGUUCUCUUACACCAUACUUGCUGAAUGCAGUGCUCG	UCG 8299 : TAA 7921
8300 GGAUUAGGGAGUUUUCAUGGAAGAUUGGGACAUAGGCGUGCAGAUGCUUCGAAAUUUGC	UGC 8359 : TAT 7981
8360 ACACUGAAAUAAUUUACACCCCCAUUGCAACACCUGAUGGAACAGUCGUCAAAAAGUUUC 	UUC 8419 :: TTA 8041
8420 GAGGAANDANAGUGGUCAACCGUCAACAGUCGUAGAUAACACAUUGAUGGUCUGUAUUUU	.UUU 8479 : TAG 8101
8480 GUGUGCAGUAVAGUUVAAUUAUGAAUAGUGUAAAGUUUGAGAAUCAGGAUGAUGUCUGCA :	GCA 8539

8984 ACTTGGCTAACACAAGGCTACAAGGAAACAATTTGACACATGGTATGATGAGGTTAAAC 9043 CTAGAGACAAGGGGAACTTTGGTCCATGTCTCATCAAGGGAAAAGAGTGGAGGACATAT 8642 ACACTACCGAACCAGAGGATTTATTTGTATATCATCAAAGTGGCGACGACACGTTGGATG 9044 GAGATTACGAGTTGGATGACAGCTCAATGCAAATAATCCTGAATGGATTGATGGTTTGGT AACCAGAACACAGAUUAGAAGCGAUUUGCGCUUCGAUGAUUGAAGCAUGGGGUUACCCUA GGUJAAUCCACGAAAUUCGAAAAUUUJAUGCUUGGGUUCUGGAACAAGCACCAUACAAUC 8462 AGCTAACTCATCAGATACGGAGGTTCTATGCATGGCTTATTGGACAAGCTCCATACTCGG GCGCAUCUGGUGCUAUUGUUUCAAACAACGAAAAAGACAAGGAUGUCGAUGUAGGAUCAA GUAUUGAAAAUGGAACAUCUCCAAACAUUAAUGGCAUGUGGUUUAUGAUGCAAGGGGAAG AACAAAUCGAAUACCCCCUUCAACCAAUAGUGGAAAACGCAAAAACCCCACUUGCGUCAGA UAGAUUCUUUUAAAGUUCAUUUUGCUAAUUUAGGUUUAGACUACGAUUUCUCUCAUCGAA CGAAAGACAAAGGAGAACUUUGGUUUAUGUCUCACAAAGGAGUUAAAUUAAAUGACAUGU 8720 AUAUUCCAAAGCUGGAGCCAGAGAGGUUGUCUCAAUACUUGAGUGGGAUAGAAGUGUAA 8960 CAUGCGAAGAAGGAAGUGCUGAUGAAAUCAUGUCAUACUU---AGAGAUGUGCAAGUG AUUUGAACGAGGAUGAUGAUGAUGAUGAUGUUUCUCACCAGUCCGCUCUUGAUG 8702 crocaacaacrecreccaagraagcaaggaagcaagaaagcaagaagcaagcrecacreaaggca GUGGAUCUTUCAUCAAACACCACGAAUTAAAUCGAUAUCCAAUAAACUCACAAUGCCAAAAG ACAUTUCAAAUACCAGGGCAAGUAUTUCACAGUUUAAUACAUGGUACAACGCUGUGAAGG AAUCCUAUGGUGUGUCUGAUGAAGAAAUGGGAAUAAUUUUGAAUGGAUUAAUGGUUUGGU 9197 (

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel attenuated virus (10-0) of sweet-potato mottling mosaic virus, having a sequence of 1980, 3960, 5940, 7980, 9960 or 10820 nucleotides, given in specification. The attenuated virus (10-0) is capable of inducing cross protection for the sweet-potato mottling mosaic virus high virulence strain, which is a pathogen causing sweet-potato banded russet disease. The invention further comprises: a mottling mosaic virus high virulence strain resistant sweet-potato obtained by inoculating the attenuated virus (10-0); and a mottling mosaic virus high virulence strain resistant sweet-potato, obtained by carrying out the vegetative propagation of one part of mottling mosaic virus high
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New attenuated virus (10-0) of sweet-potato mottling mosaic virus, capable of inducing cross protection for sweet-potato mottling mosaic virus high virulence strain causing sweet-potato banded russet disease.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Attenuated virus (10-0); sweet-potato mottling mosaic virus; cross protection; sweet-potato banded russet disease; virucide;
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DOKURITSU GYOSEI HOJIN
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virulence strain resistant sweet-potato. The attenuated virus (10-0) has virucide activity. The attenuated virus (10-0) is useful for preventing sweet-potato banded russet disease, which involves inceulating a sweet-potato with the attenuated virus (10-0). The attenuated virus (10-0) is safe, cost-effective and also does not cause environmental pollution. The protective effect of attenuated virus (10-0) against sweet-potato banded russet disease, is also carried to the next generation. This
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Best Local Similarity 54.0%; Score 2117.8; DB 13; Length 10820;
Matches 4675; Conservative 0; Mismatches 3850، تسطماء 10.2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 10820 BP; 3507 A; 1983 C; 2563 G; 0 T; 2764 U; 3 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The present invention describes a gene expression vector for plants of the Lemuginosae or Nicotiana genus of Solanaceae or the Gladiolus genus of Iridaceae, comprishing a cDNA against the genome of a Clover yellow vein virus. Also described are: (1) a bacterial host transformed by the gene expression vector in a plant; and (2) a transformed plant in which an exotic gene is introduced by the gene expression vector into a plant. The gene expression vector can be used for creating a useful plant highly resistant to environmental stresses. The present sequence represents a clover yellow yein virus gene which is used in an example from the
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green fluorescent protein; environmental stress; ds
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HOKUREN NOGYO KYODO KUMIAI.
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648	6480 GGAAUUAGUGCAAGCUCAUUUCGGAGAAAUCAGAGAAAAUGCUAGAGAGGCCUCAU 6539 ::	oy O	
654	6540 CGAUAGGCAACACCUCUUAAAUAAACCAGGUUUGACAGCAUACUUAGUUAAGGACGGGU 6599 	oy O	7614 GUUUGAAUUGUAUCUGCAACUCGU
660	6600 UAAGUCCAUCAUGAAAGUAGAUUGCAACCACACACCUCUACUCAUAUGCAAAAACAA 6659 : :	oy Op	
666	6660 AGCGACAAUAGCAGGUUUCCUGAGAAGGAGUUUGUUUGGACAAAACGGACAAAAGCAUA 6719 	da d	
672	6720 UGAAGUAAGUAGGAACUACCAGAACGGAAUGAAGACGUUUCUUUUGAAGG 6773 	ò a	7794 CAUCGAAAUUAUGAUGGAAC 1330 TGAGTGCTAAGACAAAAAGGG
677.	6774 AGCCUCAAGUGAAAGGGAUUGCGCGAUUACAAUGGUGUAGCCAGCGCUAUUUGCCAACU 6833 	or or	
683.	6834 CACAAACAACUCAAAUGGUCGGUCCACCACAACUUAUGGGGUUGGCUUUGGCUCAUACAU 6893 	oy Op	
689.	6894 CAUAGUUAAUAGCACUUGUUUAAAGAAAAUAAUGGGAAUUUAUUGAUCAAAUCGACGCA 6953 	ර් සි ර	
695,	6954 UGGAAAUUUCAAUAUCAGGAACUCCAAGCAAAUUAAAGUCGUCGGAGUGGAGGAGGAUGGGA 7013	os da	8034 AAUUGAAAGGUUGAAGCAAACAAA
701,		op ox	
707.		රි සි රි	8154 AUGCCCAUGGACACUCGGAUGACU :
713.	1134 UGCAAGCAUUCGGAGACAAGCAAAACAUUCCCACGAGUUGAAGGUAGUUUUGGAA 7193 	୍ ପ	

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6189 7313 6069 7253 7433 6969 7493 7089 7613 7673 7209 7329 7913 8033 7689 UAAGUUUUAUUGCGGAUGGAAUGUUCUUCUAGGUAA 8213 || ::::|:|| || :|| :::| || ::::| | || :|| || :::| | CAAATITTATGGTGGGATTCATTGTTGAATAA 7749 UUAUAUUAACAAGUUGAAGGAACUGAAAUGGGAGCA 7373 ||| :| || :| || || : |CAAGATGGCAAGCCTTCTTAGTGATTTGAATTGTTC 7029 7553 7269 7853 7389 || || || GAAGAATTTGCCAAATTCATTAGAGCAAGTTGTGA 7509 UGAUUUCAACAACCAAUUUUAUGAUCUUAAUAUGAA 8153 CAAGGAAGCAUACAUUAAGGACCUAUUUAAAUACUC 7733 rcaacacudagaduurgaagaugcaguugggcaagu 7793 AACGCGAACAUUCACAGCAGCUCCAAUUGAAACUUU 8093 UGAUGAUCGAAAUCAUTUGCUACAGCUUAGUUGUCU 7973 CCAGGAGGCAGAAAATTCTTTAGACCTATGATGGG TGCTTCATTGACAGGCACGTTAACATCTTCACAAG ACAUUGUGGAUUGCCUUUAGUUAGUGUCACUGAUGG IAAUGAGUCADAAGDACGAUCADAAUDAUUUCUCGAA UNANGUUGAUUNAGCGACUUNAUGCACGGAACCUGUGUG UGUUACAAAGCACAUUGUGAAAGGACGAUGUAAAUU CUUDAGGGAAUGCAAGUADAUCACCGAUUGUGACCA AAUTUGGAAUGGAAGUCUUAAAGCUGAAUUAAGACC ugunagunggggcaacaugaaacuncagganagugc AUGGUDAUANCAGCUUGAAGGAAAUUUGAAAGC UAGUGAAGCGAAUGAGUUCUUUAAACCACUGAUGGG AGCGGCAGUCGGUGCGUUGUACAGUGGUAAGAAAA

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9474 UUUGAAUGGAUUAAUGGUUUGGUGUAUUGAAAAUGGAACAUCUCCAAACAUUAAUGGCAU 9533
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Etch Virus; TEV; large nuclear inclusion protein; capsid protein; transformation; Agrobacterium tumefaciens; potyvirus; ss.
                                                                                                                                                                                                                                                                          9594 CGCAAAACCCACUUUGCGUCAGAUUAUGGCUCACUUUAGCAAUGUUGCUGAAGCAUACAU
                                                                                                9414 DACAUGGDACAACGCUGUGAAGGAAUCCUAUGGUGUGUCUGAUGAAGAAAUGGGAAUAAU
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/note= "Undetermined residue"
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/*tag= 3b
/note= "Large ORF encoding large nuclear inclusion
protein and capsid protein"
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/note= "TEV coat protein"
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                                                                                                       | : | | | | | | AGTGCACCAAGTCATGTATCTAGACCTTTCTACACTTTTCAAAGAGTTGGG 8166
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            AGGCGUGCAGAUGCUUCGAAAUUUGCACACUGAAAUAAUUUACACCCCCAUUGCAACACC
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                                                                                                                                                                                                                         This sequence represents a fragment of the Tobacco Etch Virus (TEV) genome which contains the largest ORF in the third reading frame. The protein product of this ORF is cleaved to give the large (54 KD) nuclear inclusion protein and the capsid protein. This plus strand was used as basis in the construction of a vector suitable for transformation into Agrobacterium tumefaciens (AT) cells. The vector constructs of the invention (see also AAQ5565-67) represent a full length coat protein gene, a truncated coat protein gene and an antisense coat protein gene. The resultant transformed AT cells may be used to transform cultured tobacco cells. The transformed cells had reduced susceptibility to viral infection, ie. they were resistant to potyvirus infection. (Updated on 25-MAR-2003 to correct PN field.)
                                                                                                                                                            Plant transformation vector - comprising tobacco etch virus-derived mutated gene, conferring viral resistance to e.g. tobacco plants infected
                                                                                                                                                                                                                                                                                                                                                                                                                                                      1091 CATACTCTAAGAAATTCTTGGAGTTGAGA-CCAGATGGAATCTCCCATGAGTGTACAAGA
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                                                                                                                                                                                                                                                                                                                                                                                  Sequence 9495 BP; 2977 A; 1816 C; 2283 G; 2418 T; 0 U; 1 Other;
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4599 4419 3900 4479 4539 4020 4080 4659 4140 4719 4200 4779 4320 4899 4380 5019 5139 4620 5199 SAAACAACCAUUGAUTUUCGACUUAGAUUGUGAGGGGAGCAAAGUUACAGAGUUC 4239 JUCCACACACACCAUCCAGUTUCCAUUCAUAUAGAGGAACAACUUAGUTUCCAA 4839 SUGUAUGUUGCUAGUUACAAUGAGGUUGAUCAGCUCUCAAAAAUGCUCGGAGAU 4959 acaaragagcggracagracaacaaacrgrggggggggraaragggagcgcarc 4680 5260 AUUAAAGGAUUGAUUGAGUUCCUAGUCUUGUGGCGACACAGGCUGCAUUUCAAUGCUUC 5319 TUGAGAAUGCGAGGAAUGUCAUCUTUUGGAUCUAGUAUAUAUAUGUAUAAUGACU JUNGCUUUCAAUUACUUNGCAAAUAAUCCUCUAAAAUUAAGUGAUUUUGAAUUU CUCUAGAUGUAGAUGUGUGUGGACUUUGGUUUGAAAGUCACUGCUGAAAUU NGAACUTUGCCGCAUGGUGGGAAAAACAACUACAAUGUGAUAGAGUGGUACCC GAACCACUGGGAAAUUUAUUGAAUUCACUCGUGAAAGCUGUGUUAGUGUGAGU ACUGGUCUACCAUUCGCGUUAUCUAGUAAAGGCGCAGUUCUUAUGCUCGAACCA CAUUGGCAGAGAAUGUCUCACGACAGUUGAGACAACAUCCCUUUUAUGCAAAC BACAACCGGUGCGUUAAUUACACAAAGACCAGCAUUUCAUACGGAGAACGCAUA TUGGGCAGGGUUGGUAGACACAAAAAGGGCAUGCAAUGGAAUUGGAACUACA rcegracaerreseccaeaeaeaaeaaeaaearaeeaerresaarresecaaaea NUAUCUCAUGCCCCUGAGAAGAAUGGAUAGUCCGUGGUGGUGGUGGAUCAGGA

5818 AAGCGCAAGGGCACCACGAGAGAA 6394 GGAGUUAAUUACAAGAUUUGCUU 6454 CGUGAUGAGCACCTGATTTTTCAT 6454 CGUGAUGAGAGCCCUUGACAGAG 6514 GACAAAGGCCACAAACGCACCTA 6514 GACAAAUGCUAGACGAGGCCUCA 6514 ACACGAUGAGAGAGGCGGCGCCGC 6574 ACACGAUACUUAGUUAAGGAGGGG 7 6574 ACACCAUATTGGTGAATAGGGGG	6634 AAUCCUCUACUCAUAGGAAAAGA 6118 TCGTCGCTACGTGCGAGTGAGAAT 6694 GUUUGCGACAAAGGACAAGGACAAAGGACAAGGACAAAGGACAAGGACAAGGACAAGGACAAGGAGAAAAGGAGAAGGACTTAGAGAAAAAGGAGAAAAGGACTAAGGACTTAGAGAAAAAGGACTAAGAGAAAAAGGACTAAGAGAAAAAGGACTAAGAGAAAAAGGACTAAGAGAAAAAGGACTAAGAGAAAAAGGACTAAGAGAAAAAGGAACTAAGAGAAAAAGGAACTAAGAGAAAAAGGAACTAAGACAAATAGACGACAATTGACAATTGACGACTATAGAGGAAGGA		7114 ACGUUCCAAGAAAAGUACAAUGCAA :-
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	8734 GAGCCAG 8200 GAAGAAG 8794 UUAGAAG 8260 CTTCAAGA 8854 AUUCGAA 8320 ATCCGCA		9094 GAAAACA 8530 GATGCTG 9154 AAAAAUA 9157 AAAGATC 9214 GUUUCAA 8595 9274 CCACGAA 9274 CCACGAA	9334 UNANUU 934 GCAAGUN 9394 GCAAGUN 9761 GCCACAC 9454 GAUGAAG 9821 GAAGACG 9514 UCUCCAA 9514 UCUCCAA 9514 UCUCCAA 9514 UCUCCAA 9514 UCUCCAA 9514 UCUCCAA 9514 UCUCCAA 9514 UCUCCAA 9514 UCUCCAA 9514 UCUCAAC
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                                                                                                                                                                                                                                                                  GGUAUUCAACGGAACCUCACCGACAUGAGUUUGGCGCGAUAUGCUUUUGAUUUCUAUGAA
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                                            1415 GGAGAGGGCACAGUGGACAUAUCAUUCAAUAUGAUAAGUUUAGAGGUUUGAGUGGACGGC
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DB 2; Length 9705;

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Score :

19.9%;

Query Match Best Local Similarity

	3704 GGUGCUUGCCUGAUI 3204 GGCGUUUGCCAACCI 3764 GCGUUUGGCAUUCAC			4118 UUGCCACAUGUGAUC 3624 UUUCCUCACUGGAUL 4178 CUGACAAGAAAAAAAAAGAAAGAAAGAAAGAAAGAAAGAA	3804 CACAUJACAGACUC 4358 GUAACACAAUAUCUC 4318 GAAAUCUACUCGCC 4118 GAAAAUCAACUGGCC 4178 CAAAGUCAACUGGCC 4178 CAAAGUCAACUGGCC 4178 CAACGCCACUGGCC 4178 CAACGCCACUGGCC 4178 CAACGCCACUGGCC 4178 ACCCCACUUGAGA 4538 ACCCCACUUGAGA 4538 ACCCCACUUGAGA 4538 CCCCACUUGAGA 4538 CCCCACUUGAGA 4598 CUAGUGGAUUCGCCC 4598 CUAGUGGAUUCGCCC
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			AUGACUUGGAUCGGAGCUGAAACAUUAUUAGUAGGUGGAGACCUCCAUAGCAAGCA		a AGCAGAGACUAAUACUUGAACGGGGGCGCAAUUUGAUUUCGGUCAUGGAAACCAUAC 3283
Qy 2495 Db 1947 Qy 2555 Db 2007 Qy 2612 Db 2067 Db 2067			Qy 2912 Db 2367 Qy 2972 Db 2427 Qy 2989 Db 2487		Oy 3224 Oy 3284 Oy 3344 Oy 3344 Oy 3346 Oy 3464 Ob 2966

CGAGAAAGUUCUGAUGAAUAAUUUAGUGGCCCUUCAUAAGGAGCAGA 3880 3443 AGCUAAUUCUAUAUCGUUCGACUAUGCACAAAUGAAGAGAGAAA--- 3820 AGACCUGACAAAGGAAUUUAAGGAGUACAUUGCAAGAAGUAGAC 3940 4237 AGGCGCUACCGAUUVAGGCGGUCGAUAUUCAGUAUCUGCAAAGCAGU 3583 SAUGAAACCUGUCAAGAAUCUUGUGUAAAAGCAAGAGAUACUUGUA 3643 agecea a de contra de cont CAAUACAACAUCCUGGACAUUUCGGGCAACAUUUUCUUUGUGUAGGU 3703 vacuaagugugaaavauuvcauccuuruvcauvcgaagaaucuura 3203 cturcucacuturetuaacucautatuaktuatuaduatuaaca 3263 AUVAGUVAAUAAAGAAUUGCAAGAA---GAAGUUGAUCAUCAAGCUA 3997 ACAAAACUUGGAGAAAAUUAUAGCAUUUGUUGCCUUAGUUAUGAUGA 4057 SARARGUGAUJGUGUAUAUAAGACACUGAACAAAUJGCGAAAUCUCG 4117 JGAACCUGUCGCACAUCAAAGCUUGGACGACAUUCAAGACAUCUUGA 4177 juaugaagijuagacaucaguccijuagacgauguggaugaagaaujutg 3683 CUUUGCCGCAUGGUGGGAAAAAAACAACUACAAUGUGAUAGAGUGGUAC 4297 CACUGGGAAAUUUAUUGAAUUCACUCGUGAAAGCUGUGUUAGUGUGA 4357 JCUACCAUUCGCGUUAUCUAGUAAAGGCGCAGUUCUUAUGCUCGAAC 4477 swieceueincaucinaeieueeceeaucueieecinnaaeueaae 3983 sechenendeucuchen ach de la 1888 adcegadaaceuuuucaaacadcuaucuagugaaccauucuucaaga 4043 AAUGCGAGGAAUGUCAUCUUUUGGAUCUAGUAAUAUAUGUAUAAUGA 4597 4598 CUAGUGGAUTUGCUTUCAAUUACUTUGCAAAUAAUCCUCUAAAAUUAAGUGAUTUUGAAU 4657 AGAAAAGGCAGAUUUGAAAGGGUUAUACAACAUAUCACCACACAGCGU canuncacauggangagacamgagunungaagucaguaaacc UGUUUGAAGUUUAUAAACAUGCUUAUAGUUAUAAGUUUGAUUCUCA AACCAUUGAUUUCGACUUAGAUUGUGAGGGGGGGCAAAGUUACAGAGU JAVGCGUGGAAAUAGUAUATTGGCUCUUCUCCAAUCUCCGUCAUGA

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8242 7754 8302 8362 8422 8482 8542 8662 8174 8722 8782 8002 8122 7634 7874 7934 8054 8602 8234 8474 3963 GCGAAGAAGGAAGUGCUGAUGAAAUCAUGUCAUACUUAGAGAUGUGUGCCAAGUGAUUUGA 9022 CAGUCGGUGCGUUGUACAGUGGUAAGAAAAAGGCGUACUUCGAAAAUUCCACAUUUGAUG egaacegaucaujgaagecagaeciceguegaagagagagagauacujgcaaauaagacga GAACAUUCACAGCUCCAAUUGAAACUUUACUUGGCGGAAAGGUUUGCGUCGAUGAUU UUUAUUGCGGAUGGAAUGAUCUUCUAGGUAAACUUCCUGAUGGUUGGAUAUACCGCGAUG CUGACGGAUCACGAUTUGACAGUUCUCUTUACACCAUACUUGCUGAAUGCAGUGCUCGGGA UVAGGGAGUTUTUTUCAUGGAAGAUTUGGGACAUAGGCGUGCAGAUGCUUCGAAAUTUUGCACA CUGAAAUAAUTUACACCCCCAUUGCAACACCUGAUGGAACAGUCGUCAAAAAGUTUCGAG GAAAUAAUAGUGGUCAACCGUCAACAGUCGUAGAUAACACAUUGAUGGUCUGUAUUUGUG 7935 GUAAUAAUAGUGGUCAACCUUCUACCGUUGUGGAUAAUUCUCUCAUGGUUGUCCUUGCUA uecaunacecucucaunaaeaagueceuusaeuureaagaauceacaceaceuguau AUUCUUUAAAGUUCAUUUUGCUAAUUUAGGUUUAGACUACGAUUUCUCUCAUCGAACGA AAGACAAAGGAGAACUUUGGUUUAUGUCUCACAAAGGAGUUAAAUUAAAUGACAUGUAUA UUCCAAAGCUGGAGCCAGAGAGGGUUGUCUCAAUACUUGAGUGGGGAUAGAAGUGUAAAAC CAGAACACAGAUUAGAAGCGAUUUGCGCUUCGAUGAUUGAAGCAUGGGGUUACCCUAGGU UAAUCCACGAAAUUCGAAAAUUUUAUGCUUGGGUUCUGGAACAAGCACCAUACAAUCAUC UCGCAUCUGAGGGAAAAGGCACCAUACAUTUCGGAAACAGCGCUCAAAAGACUUUACACAU AUCGAAAUCAUUIGCUACAGCUUAGUUGUCUCCGAUUAUUCAAGGGUGAUUUGGGAAUUU UCAACAACCAAUUUUAUGAUCUUAAUAUGAAAUGCCCAUGGACAGUCGGGAUGACUAAGU UGCAGUAUAGUUUAAUUAUGAAUAGUGUAAAGUUUGAGAAUCAGGAUGAUGUCUGCAGGU

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                                                  9023 ACGAGGAUGAGUACUUUGAUGAUGAUGAUGUUCUCACCAGUCCGCUCUUGAUGCUGGCA
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AAQ35297 standard; DNA; 9593 BP.

RESULT 7

AAQ35297

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This sequence represents the nucleotide sequence of the zuchini yellow mosiac virus (ZYMV) genome. ZYMV is a potyvirus and expresses its genome as a single 350 kD polyprotein which is cleaved into at least seven mature gene products by three distinct proteolytic activities. Two of the proteases are virus encoded, including the potyviral 49 kD protease. This protease is responsible for at least five of the seven cleavages. This enzyme is a trypsin-like cysteine protease which is structurally and mechanistically representative of the largest class of viral proteases,
                                                                                                                                                   /*tag= a
140. .9382
/*tag= b
2437. .2438
/*tag= //tag= component (HC) and the 46 kD protein"
/*tag= //ote= "Cleavage site between aphid transmission helper/component (HC) and the 46 kD protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        od for identifying protease inhibitors - useful for drugs screening treating e.g. chronic inflammation, metastatic cancers and viral
                                                                                                                                                                                                                                                                                                                                                                                                                              coat protein
                                                                              Zuchini yellow mosiac virus; ZYMV; potyvirus; polyprotein; protease; proteolytic activity; 49 kD protease; trypsin-like cysteine protease; animal picornavirus; sissile bond; NIb; protein; coat; ss.
                                                                                                                                                                                                                                                                                                                                 CI and VPg/protease
separated in ZYMV)"
                                                                                                                                                                                                                                                                                   and
                                                                                                                                                                                                                                                                                                                                                                               between VPg/protease and
                                                                                                                                                                                                                                                                                  between 46 kD protein protein (CI)"
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/note= "Polyprotein termination point"
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                                                                                                                                                                                                                                                                                                                                                                                /note= "Cleavage site
replicase (REP)"
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"Cleavage
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                                 (first entry)
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P-PSDB; AAR35081.
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                     25-MAR-2003
28-MAY-1993
                                                         ZYMV genome
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                                                   amino
                                      specific and appears to recognise a region comprised of about seven amino acids surrounding the sissile bond. Of the five sites cleaved by this enzyme, the two flanking the protease appear to be cleaved intramolecularly, while the remaining three appear to be cleaved intermolcularly. Of the latter three, the site between the NID protein and the coat protein appears to be the most active. The polyprotein sequence encoded by this genome is not given in the specification but is deduced in ARR35081. (Updated on 25-MAR-2003 to correct PN field.)
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including
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The sequence of the polycistronic messenger RNA of maize dwarf mosaic virus strain B (MDWV-B) is given in AAT47073 and the encoded MDWV-B polyprotein in AAW10344. New chimaeric genes (see also AAT47074) comprise a monocotyledonous plant promoter linked to a modified nucleic acid sequence derived from the MDWV-B genome. The modified nucleic acid mRNA is translated to a truncated protein (pref. smaller than 200 amino acids), no translation of mRNA occurs or the transcribed mRNA lacks the translation initiation codon or includes a premature stop codon. Expression of the chimaeric gene inhibits infection of plants (pref. sorghum, sugarcane, esp. maize) by MDWV. The transgenic plants display an inheritable resistance trait. (Updated on 17-OCT-2003 to standardise OS field)
      MDMV-B; viral resistance; disease resistance; transgenic plant; monocot; P3 proteinase; NIa proteinase; NIb replicase; RNA-dependent RNA polymerase; coat protein; Zea mays; sorghum; sugarcane; Saccharum officinale; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Chimaeric gene for imparting viral resistance to plants - contains sequence modified to express non-translatable mRNA, or non-coat viral
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2290 AUGCGAGUCAACCCAAAUGGCACAAGACAAACAGCUAUAGGAAAACUGAUUUAUCGACG 2350 GAUCCAUCUACGCUACGACAACAAAUGAAAGGUAGCCCAAUCACAAGGGUUCCAGUUGGU 531 GACUUUCAAAAGAUUAGAGAAUCAUUCGUUGGACUCUCGGUAAAUAGACAACCGCUGGAU AAAUAUUGUACAAGCAAAAGAGAUGGUUGUUACGUCUAUCCAGCAUGCUGUGUUACAAUG 591 AAAUGUUGUGUUAGCAAGAUCGAAGGAGGGUAUAUAUACCCCAUGUUGCUGCGUCACAACA GAAGAUGGUACGCCAUUGUJUUCUGAUAUCAAGAUGCCAACUAAGAAUCAUCUAGUCAUU 651 GAAUUUGGUAAACCAGCAUACUCUGAGAUAAUACCUCCAACGAAAGGGGCAUAUAACAAUA 2530 GGAAAUUCAGGAGAUCCAAAGUAUGUGGAUGUACCA--AGCAGCUCAAGUGACAUGAUU

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291 UUGGAAUCUUUUNGAAAAUAAAAUAUCACCAAAGAGUACAAUAAAUGCGGCUUUAAUGUGC

2110 AUUCACCAUUUCCGAAAUAAGAUGUCAGGUAAAGCACAAUUUAAUUUUGCAUUGAUGUGU

2170 GACAACCAACUUGACAAAAAUGGUAACTUCGUGUGGGGUGAAAGAGGUUAUCAUGCGAAG 351 GAUAAUCAAUUGGAUAAAAAUGCAAAUUUUGUAUGGGGUAAUAGGGAAUACCACGCCAAA 2330 AGGUUUUCUUAAACUUCUUGAGAAAGUUGAUUCAACUGACGGUUAUAAGAAACACAUA 2349

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Sequence 8543 BP; 2913 A; 1637 C; 1820 G; 0 T; 2160 U; 13 Other;

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	4600 UUGGACUCGGUGUAAGCAGAAAUUCCAUAUGAUGUACGGUUUCGAUCCCCAGAGA 6413 UUGCUUUDAUUAGAUAAUACAAGACUCCAUAAGAGAGAGAGAGAGAGA	4 6533 4 780 6 593 6 893	6653 AAAACAAAGCGACAAUAGCAGGUUUCCUGAGAAGGAGUUUGUUU	6770 5017 6830 5077	6890 ACAUCAUAGUUAAUAGGCACUUGUUUAAAGAAAAUUAUGGGAAUUUGAUCAAAUUGA 6949	7010 GGGAUAUUGCCAUUCUUCAAAUGCCUAAAGACUUCCCACCCUUUGCACAGAGGUUACGAU 7069	1130 ACAAUGCAAGCAUCGUUUCUGAGACAAACAUUCCCACGAGUUGAAGGUAGUUUU 7189
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                                                                                  The sequences given in AAT64557-50 represent the RNA and cDNA from the papaya malformed leaf mosaic virus (PLDMV) coat protein gene. These sequences may be used to form transgenic plants which are resistant to PLDMV infection. Plants such as this are important in industry. (Updated on 27-AUG-2003 to correct OS field.)
                                                                                                                                                                                                                                                                                                            471 AAUUUGAAUGGAUUAAUGGUUUGGUGUUGAAAAUGGAACAUCUCCAAACAUUAAUGG
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721 AATTIGAAIGGATIAAIGGTITIGGIGIAITGAAAAIGGAACAICICCAAACAITAAIGG
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                                                                                                                                                                             Length 1404;
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                                                                Claim 2; Page 5; 6pp; Japanese
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Best Local Similarity 100.0%; Pred. No. 4.6e-306;
Matches 1404; Conservative 0; Mismatches 0; Indels
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   (NORQ ) NORINSUISANSHO KOKUSAI NORIN SUISANGYO
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/product= "PLDMV coat protein"
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                                          CAUGUGGUUUAVGAUGCAAGGGGAAGAACAAAUCGAAUACCCCCCUUCAACCAAUAGA
                                                                                                           CAUCGAAAAGAGAAAUUAUGAGAAGCCAUAUAUGCCGAGGUACGGUAUUCAACGGAACCU
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               CAUGUGGUUUAUGAUGCAAGGGGAAGAACAAAUCGAAUACCCCCUUCAACCAAUAGUGGA
                                                                                    AAACGCAAAACCCACUUGCGUCAGAUUAUGGCUCACUUUAGCAAUGUUGCUGAAGCAUA
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    end of PVBV containing NIa-pro, NIb, and CP coding regions.

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/transl_except= (pos:511. .513, aa:Xaa)
/transl_except= (pos:589. .591, aa:Xaa)
/note= "Xaa corresponds to stop codon;
shown in AAY90279"
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This sequence represents the 3' end of the pepper vein banding virus (PVBV) RNA, and encodes part of the NIa-pro protein, as well as encoding the NIA and CP proteins. The invention relates to a recombinant DNA molecule comprising one or more DNA sequences showing at least 80* homology to the coat protein (CP) gene and/or the mutant nuclear inclusion protein b (NIA) gene optionally in combination with the 3'-untranslated region (UTR) of a polyvirus, functionally linked with regulatory sequences needed for gene expression in plant cells. The recombinant DNA is useful for producing transgenic plants, especially Capsicum frutescens and C. annum which are resistant to viral infection (Updated on 15-SEP-2003 to standardise OS field)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Recombinant DNA constructs useful in providing resistance against pepper vein banding virus in peppers comprise polyvirus coat protein and mutant nuclear inclusion protein b genes.
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/note= "encoded protein shown in AAY90277"
                                       protein shown in AAY90276"
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P-PSDB; AAY90275, AAY90276, AAY90277, AAY90279.
/*tag= c
/note= "encoded
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GCUUCCUUUGAAGGGGCCCGCAAGGGGAUUGCGGAUUACAAUGGUGUAGCCAGC	1311 CCAACCCTTCATGGGTGCGTATGGTAAGAGCCGATTGAATCGTATTGCTAAGGA 1370 7719 CCUAUUUAAAUACUCAUCAAGAAAUACCAAUGGGGAGGUCGACACUGAGGAGUUGAAGA 778 : :: :
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8735 ||:||||:|||: |GATGGGGTCACAAGGAATTATTGTATGAGAT 2510 PAGCACCAUACAUCAUCGCAUCUGAGGG 8915 SUUUGCGUCGAUGAUUUCAACAACCAAUUUA 8138 |:::||||:|||:||:||||||||||:::| STITGCGTIGAIGAITICAACAACCAGIICIA 1790 |||||:||| :| || ||||| || : CAUGGGUUACCCUAGGUUAAUCCACGAAAU 8855 CUCAAAAGACUUUACACAUGCGAAGAAGGAAG 8975 : |||||:||||||| || |: ||:|| ::|:| TTAACATGAAAGCAGCTGTTGTGTGTGTA 1550 ACATACACCCAACAGGACAAAGAGCGAATACT 1610 AAGCAAACAAAACGCGAACAUUCACAGCAGC 8078 SUCGGGAUGACUAAGUUUVAUUGCGGAUGGAA 8198 :---uucgaaauuugcacacugaaauaauuua 8375 TAATGAGGAACTTGTATGCCGAAATCATATA 2030 meaugeucueuaumeueugcaguauaeum 8495 AAUUUAUACACAUCCUAGAUUCUUUUAAAGU 8615 IGGGAUAGAAGUGUAAAACCAGAACACAGAUU 8795 IUGAACAUGAAAGCGGCAGUCGGUGCGUUGUA 7898 AUTOCCACAUTUGAUGAUCGAAAUCAUTUGCU 7958 IGGAUAUACCGCGAUGCUGACGGAUCACGAUU 8258 AUGCAGUGCUCGGGAUUAGGGAGUUUUCAU 8318 PAGGAUGAUGUCUGCAGGUAUTUCGUUAACGG 8555 AUUUCUCUCAUCGAACGAAAGACAAAGGAGA AAUUAAAUGACAUGUAUAUUCCAAAGCUGGA

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                                                       2631 AAATGATATTAATCCATACTTGAGAGCGCTCATTGAGGGAGCTAAGCGGGAAGAATTGGA
                                                                                                                          UUCAAACAACGAAAAAGACAAGGAUGUCGAUGUAGGAUCAAGUGGAUCUUUCAUACC
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                                   UGCUGAUGAAAUCAUGUCAUACUUAGAGAUGUGUGCAAGUGAUUUGAACGAGGAUGAGUA
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ribosome binding sites which were artificially ligated
the viral sequence"
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                                                                                                                                                                                        potyvirus gene; protease; plant protection;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 3923 BP; 1219 A; 712 C; 967 G; 1025 T; 0 U; 0 Other;
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ilarity 40.9%; Pred. No. 2.9e-218;
Conservative 558; Mismatches 1501;
                                                                                                                                          Potyvirus 3'PVY3.9 chimeric plasmid sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                the viral sequence"
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DNA; 3923
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                                                                                             (first entry)
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                                                                                                                                                                                        Chimeric plasmid; pot potyvirus infection;
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Matches 1491; Conserv
AAX99253 standard;
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Plum pox virus
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CCCATAGAGGCCTGCTAATCGAGGGTATGTACGTGCCAAAGCTTGAAGAAGAGAGAATTG 2465
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2736 ATGATGAGTTTGAGCTTGACTCTTATGAAGTACACCATCAAGCAATGACACTAGATGATG
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                                                                  UCUCAAUACUUGAGUGGGAUAGAAGUGUAAAACCAGAACACAGAUUAGAAGCGAUUUGCG
                                                                              CUUCGAUGAUUGAAGCAUGGGGUUACCCUAGGUUAAUCCACGAAAUUCGAAAAUUUUAUG
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                                                                              AUAAGAUGUUUGGAUGGAAAAGUCGGAAAUGCGACUGAGAACACGGAGCGCCACA
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Hammerhead; ribozyme; endoribonuclease activity; catalytic region; potyvirus; replicative strand; viral replication; infection; assembly; cell movement; symptom; resistance; plant; aphid; mite; whitefly; inducible; inhibitor; toxin gene; ss. Ignart F; Vermeulen A, WMV2 strain val3 3' region cDNA. AAX77838 standard; cDNA; 2974 97EP-00402925. 97EP-00402925. (GENE-) GENE SHEARS PTY LTD. 10-AUG-1999 (first entry) Watermelon mosaic virus Tucker W, WPI; 1999-329398/28. 03-DEC-1997; 03-DEC-1997; EP922767-A1 16-JUN-1999 Huttner E, AAX77838; AAX77838

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useful for New ribozyme capable of hybridizing to potyvirus RNA, u conferring resistance of plants to potyviral infection.

Example 1; Fig 5 bisA-D; 137pp; English

This invention describes novel nucleic acid ribozyme molecules with and card at least one at least one the teats one at least one by this invention describing region which is complementary to at least one target region of the potyvirus genomic (+) and/or replicative (-) strand CRNA. The target region does not have a GUC triplet at position 812-8124 or the puvn strain, or the equivalent triplet of other potyviruses. The ribozyme cleaves potyvirus genomic (+) strand RNA or replicative (-) strand RNA, resulting in reducing viral replication, infection, assembly, cell to cell movement and/or symptoms. The novel ribozyme is useful for providing in vivo resistance to plants against potyviral infection, cepecially the aphid-, mite- and whitefly transmitted potyviruses, including: Zucchini yellow mosaic virus (ZMWV), Watermelon mosaic virus (CWWY), Tobacco vein mottling virus (ZMWV), Tobacco etch virus (TEV), potato virus Y (PVY), Pepper mottle virus (PepWoV), Soyabean mosaic virus (SbMV), Papaya ringspot virus (RUMV), Johnson grass mosaic virus (SbMV), papaya ringspot virus (RUMV), Johnson grass mosaic virus (GSWV), papaya ringspot virus (RUMV), Johnson grass mosaic virus (GSWV), and Sugarcane mosaic (SWWV), mand sugarcane mosaic (SWWV) (CEATALION vein mosaic (BYWV), CEATALION vein mottle (CEVWV), Lettuce mosaic (PCWV), CHWV), and Sugarcane mosaic (SWWV) (SWPOC) (CEWV), and Sugarcane mosaic (SWWV) (SWPOC) (LEWV), and Sugarcane mosaic (SWWV) (SWPOC) (CEWV), clover yellow vein (CIVVV), Henbane mosaic (HWV), clery mosaic ciruducible ribozyme gene is useful for inhibiting action of a therapeutic gene if it was necessary, especially useful when using toxin genes, and a synthetic ribozyme could be used to control activity of a therapeutic

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                         ACAAAAGATAACAAAAGAAAATGAACCTTCCAACAGTTGGTGGGAAAATCATTCTTAGCTT
                                                             ||:||| : |:: :|||:|| : |:||:|| | AATGGGTTGATAACGGTACATCTCCAGA
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This introlled a destribes move interest and allocated with the condition of the potyvirus genomic (+) and/or replicative (-) strand RNA. The target region of the potyvirus genomic (+) and/or replicative (-) strand RNA. The target region does not have a GUC triplet at position 812-8124 of the PVYN strain, or the equivalent triplet of other potyviruses. The tribozyme cleaves potyvirus genomic (+) strand RNA or replicative (-) strand RNA, resulting in reducing viral replication infection, assembly, cell to cell movement and/or symptome. The novel ribozyme is useful for providing in vivo resistance to plants against potyviral infection, especially the aphid-, mite- and whitefly transmitted potyviruses, including: Zucchini yellow mosaic to plants against potyviral infection, especially the aphid-, mite- and whitefly transmitted potyviruses, including: Zucchini yellow mosaic (TWWV). Tobacco etch virus (TEV), potato virus (TWW), Papara ingspot virus (TWWV), Johnson grass mosaic virus (GEWV), Papaya ringspot virus (TWWV), Johnson grass mosaic virus (JGWV), Ban common mosaic virus (SEWW), Bean common mosaic virus (CEWW), Clover yellow vein (CIVW), Henbane mosaic (HWV), Lettuce mosaic (CEWW), Boarcane mosaic (SCWW) (especially ZYW and WWV2). An inducible ribozyme gene is useful for inhibiting action of a therapeutic gene if it was necessary, especially useful when using toxin genes, and a synthetic ribozyme could be used to control activity of a therapeutic
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                                                                                                                                                                                                                                                     This invention describes novel nucleic acid ribozyme molecules with
                                                                     useful for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         51;
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                                                                 New ribozyme capable of hybridizing to potyvirus RNA, u conferring resistance of plants to potyviral infection.
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8.4%; Score 854.8; DB 2;
Best Local Similarity 41.7%; Pred. No. 4.4e-182;
Matches 1144; Conservative 450; Mismatches 1097;
                                                                                                                                                                                    Example 1; Fig 5A-D; 137pp; English.
WPI; 1999-329398/28
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UGCGAAUAAUAAGAUGUUUGGACUGGAUGGAAAAGUCGGAAAUGCGACUGAGAACACGGA CAACGAAAAAGACAAGGAUGUCGAUGUAGGAUCAAGUGGAUCUUUCAUCAUACCACGAAU GGAGUUCCUUUUACAAUACACACAGAUCAAGUGGACAUUUCAAAUACCAGGGCAAGUAU |||||||::: | ||:||:||| ||: || || acacagitigaatacgaitcttaacgaitgagca UGAAGCAUACAUCGAAAAAGAGAAAUUAUGAGAAGCCAUAUAUGCCGAGGUACGGUAUUCA AAGGACGCCAGCUCGGGCCCCGGGAAGCCCACAUCCAGAUGAAAGCUGCAGCAUUGCGAGA GAUTUGCGCUTUCGAUGAUTGAAGCAUGGGGUTAACCCUAGGUTAAUCCACGAAAUTUCGAAA AUTOTO A UN TO CONCOGRACIA CON CANCONCOCCANCO CANCO CAN Accauacauurcegaaacaececucaaaaeacuuuacacauecgaagaaegaaeuecuea UGAAAUCAUGUCAUACUUAGAGAUGUGUGCAAGUGAUTUUGAACGAGGAUGAGUACUUUGA :||| : | | | | : | | : | TGAATTGCAAAAATACCTGGAGTTTTAACCACTGATGGTTGCTG-----UGAUGAAGAUGUUUCUCACCAGUCCGCUCUUGAUGCUGGCAAACCCCACAGCAGAAAAAAA GAAAGACGAUGAAGAAGAAAGAAUAAAGAAGAAAAAGCAGGAAAAUAAAAACAAAAAUAA GGACTCGAAGAAGGACACCCAGTGGCAAAGGGGATAAGCCACAAAATTCGCAAACTGGTCA AGAAGUCGAGAAGAAACAUGAGAAAACUUCGAAUAGCGCAUCUGGUGCUAUUGUUUCAAA UAAAUCGAUAUCCAAUAAACUCACAAUGCCAAAAGUGAAAGGGAAAGGAAUUUUAAAUUU ACAAAAAGATAACAAAAGAAATGAACCTTCCAACAGTTGGTGGGAAAATCATTCTTAGCTT UUCACAGUUUAAUACAUGGUACAACGCUGUGAAGGAAUCCUAUGGUGUGUCUGAUGAAGA AAUGGGAAUAAUUUUGAAUGGAUUAAUGGUUUUGGUGUAUUGAAAAUGGAACAUCUCCAAA CAUUAAUGGCAUGUGGUUUAUGAUGCAAGGGGAAGAACAAAUCGAAUACCCCCUUCAACC AAUAGUGGAAAACGCAAAACCCACUUUGCGUCAGAUUAUGGCUCACUUUAGCAAUGUUGC g ò GAGGGUUGUCUCAAUACUUGAGUGGGAUAGAAGUGUAAAACCAGAACACAGAUUAGAAGC 8801 |::|| :|: :::|| || :::|| || || || CCTTAGCTGAGGAACTTTGGAACGTTCCTTGAAAGC : | | | | | : | : | | | | : | : | | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : | : AGGAAAGAAACAGGATTACTTTTTTGGATAGTTTTTGATAAGGAGCGCCTGTTGTA UGAAUUAAGACCAAUUGAAAAAGGUUGAAGCAAACAAAAACGCGAACAUUCACAGCAGCUCC GGAGTTGAGGCCAATTGAAAAAGTGCAGGCAAACAAAACTAGAAACATTACAGCAGCACC AAUUGAAACUUUACGCGGAAAGGUUUGCGUCGAUGAUUUCAACAACCAAUUUUAUGA AGAUUGGGACAUAGGCGUGCAGAUGCUUCGAAAUUUGCACAGUGAAAUAAUUUACACCCC CAUUGCAACACCUGAUGGAACAGUCGUCAAAAAGUUUCGAGGAAAUAAUAGUGGUCAACC UUDAUUGCUUGCAAUCAAUCCAAAAUUUAUACACAUCCUAGAUUCUUUAAAGUUCAUUU TATTATCTTGGCAGTTAGGGATGAGGATGTGTGGCTGTATGACACTCTAAGTGCTTCATT UGCUAAUTUVAGGUUUAGACUACGAUTUCUCUCAUCGAACGAAAGACAAAGGAGAACUUUG AUTUDAAAUACUCAUCAGAAAUACCAAUUGGGGAGGUCGACACUGAGAGAUUUGAAGAUGC AGUUGGGCAAGUCAUCGAAAUUAUGAUGCAAUGGAACUUUAGGGAAUGCAAGUAUAUCAC UGGUAAGAAAAAGGCGUACUUCGAAAAUUCCACAUUUGAUGAUCGAAAUCAUUUGCUACA GCUDAGUUGUCUCCGAUUAUUCAAGGGUGAUUUGGGAAUUUGGAAUGGAAGUCUUAAAGC UCUUCUAGGUAAACUUCCUGAUGGUUGGAUAUACCGCGAUGCUGACGGAUCACGAUUUGA GUJUAUGUCUCACAAAGGAGUJAAAUJJAAAUGACAUGUAUAUJUCCAAAAGCUGGAGCCAGA

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This invention describes novel nucleic acid ribozyme molecules with endoribonuclease activity, comprising at least one catalytic region, and at least one hybridizing region which is complementary to at least one target region of the potyvirus genomic (+) and/or replicative (-) strand RNA. The target region does not have a GUC triplet at position 8122-8124 of the PVVN strain, or the equivalent triplet of other potyviruses. The ribozyme cleaves potyvirus genomic (+) strand RNA, resulting in reducing viral replication, infection, assembly, cell to cell movement and/or symptoms. The novel ribozyme is useful for providing in vivo resistance to plante against potyviral infection, especially the aphid. Mite- and whitefly transmitted potyviruses, including: Zucchini yellow mosaic virus (ZYMV), Watermelon mosaic virus (FDMV), Pepper mottle virus (PEMWV), Tobacco etch virus (TEV), Potato virus (PVV), Pepper mottle virus (PEMWV), Potaper mottle virus (PEMWV), Donam mosaic virus (FDMV), Maize Dwarf Virus (MDV), Bean common mosaic (PCMV), Plum pox virus (PBVW), Carnation vein mottle (CarWWV), Celery mosaic (LEWW), and Sugarcane mosaic (SCWV) (especially ZYWV and WMVV). An
2596 AATTAACAGCAGGTTATTTGGGCTTGATGGTAATATCTCGACCAATTCCGAAAATACTGA 2655
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                                                                                                                                                                                                                                                                                                                           Hammerhead; ribozyme; endoribonuclease activity; catalytic region; potyvirus; replicative strand; viral replication; infection; assembly; cell movement; symptom; resistance; plant; aphid; mite; whitefly; inducible; inhibitor; toxin gene; ss.
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                                      GCGCCACACCGCAGACGAUGUDAACCAUAACACUCAUGCAUU 9923
                                                          GAGGCACACTGCAAGGGACGTGAATCAGAATATGCATACTTT 2697
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Query Match 8.1%; Score 818.2; DB 2; Length 2922; Best Local Similarity 42.1%; Pred. No. 7.8e-174; Matches 1157; Conservative 451; Mismatches 1083; Indels 60;

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is funded by NSF's Plant Genome Research Program
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BI699497 sag37f04.
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BEG908772 sac9106.
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/nctom="Vector: pseudostrip; Site 1: Sal1; Site 2: Not1; This const library was constructed_from mRNA isolated from seed coats (100-20mgs) of greenhouse grown plants. The library was prepared using the Life Technologies psuperscript cDNA library construction kit. Complimentary DNA was synthesized from mRNA using a poly (dT) sequence with a Not I restrictions site. Sal I linkers adapers were ligated to the blunt-ended cDNA fragments followed by Not I digestion. The cDNA fragments were directionally cloned into the Not I-Sal I restriction site of the psoPoRTI vector. The ligated cDNA fragments were transformed into E.coli Electromax DH10B host cells. This library was constructed by Dr. Lila Vodkin and Dr. Anu
                                                                                                                                                                                                                                                                                                                                              Email: estewatson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTB on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stope: 446.
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Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M., McCann,R., Waterston,R. and Wilson,R.
Public Scybean EST Project
Unpublished (1999)
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/lab host="DH10B"
                                                                                                                                                                                                                                4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA Tel: 314 286 1800
Fax: 314 286 1810
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2.8%; Score 289; DB 5; Length 63
Best Local Similarity 47.3%; Pred. No. 4.7e-58;
Matches 292; Conservative 120; Mismatches 205; Indels
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/clone="SOYBEAN CLONE ID: Gm-c1023-5139"
                                                                                                                                                 Project
                                                                                                                                                                                                              Washington University School of Medicine
                                                                                                                                          Contact: Shoemaker R/Public Soybean EST
Public Soybean EST Project
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/cultivar="T157"
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          þe
          (DBI-0115684). More information about the project can obtained at http://fgp.bio.psu.edu"
                                                                                                                                                                                                                                                                                                                                9534 GUGGUUUAUGAUGCAAGGGGAAGAACAAAUCGAAUACCCCCUUCAACCAAUAGUGGAAAA
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99; Mismatches 224; Indels
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When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
Insert Length: 1010 Std Error: 0.00
High quality sequence stop: 421.
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Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCann, R., Materston, R. and Wilson, R.,
Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                                                                    8496
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/note="Vector: pBluescript II SK+; Site 1: EcoRI; Site_2:
Xho1; The cDNA library was constructed from floral
meristematic mRNA provided by Dr. Halina Knap of Clemson
University. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                          || || || := | || || || || || || || || acaccaattctaaggaaacaacagtggg
ATGGAAGACTGGTGGGTTGGAAGAGAAATGCTAGAGAACCTCTATGCTGAGATAGTCTAC
                                                                                                                                                                                                                                                |||||| :| |||||| |: || || || :: || :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||
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                                                                                ACCCCCAUUGCAACACCUGAUGGAACAGUCGAAAAAAUUCGAGGAAAUAAUAGUGGU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        541 TGTAAACAAGGGTGGTCAGAGGACATTCAGGAAAGATTAGTGGTTTTCGCCCATGGC
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|clone="GBNOME SYSTEMS CLONE ID: Gm-c106
| Clone="type="floral meristematic mRNA"
|lab_host="DH10B"
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/cultivar="Corolla"
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BF423562.1 GI:11411551
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Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theisting, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
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                                                                                                                                                                                                                                                                                                                                                                61
cDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. T ligated cDNA fragments were transformed into DH10B host cells (GibcoBKL). This library was constructed in the laboratory of Dr. Randy Shoemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                   62 CAACAAGAACACAATTCGAAGCGTGGTACAATGCAGTTAAAGATGAAGATGTGACG
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                                                                                                                                                                                               2.6%; Score 260.4; DB 2; 49.5%; Pred. No. 3.6e-51;
                                                                                                                                                                                                                                                      94; Mismatches 196;
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Fax: 315 286 1810
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Unpublished (1999)
Public Soybean EST Project
Public Soybean EST Project
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                                                                                                                                                                           303 GGAAAATGCAAAACCAACTITGAGACAAATCATGCACCATTTCTCAGATGCAGCAGAAGC 362
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Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I; Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                                                                                                                                                             243 TGGCGTGTGGGGTGATGAATGGAGAAGAACAGATTGAATATCCGCTGAAACCATTGT
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                                                                                                                                9468 AAUAAUUUUGAAUGGAUUAAUGGUUUGGUGUAUUGAAAAUGGAACAUCUCCAAACAUUAA
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                         Public Soybean EST Project

Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project

Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone): 800 423 4163; email: info@biogeneticservices.com)
Seq primer: -40RP from Gibco
High quality sequence stop: 426.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /done lib="Gam-cl08"
//note="Wector: pBluescript II SK+; Site_1: EcoRI; Site_2: Xhoi; The mRNA was isolated from rootes of 7 day old "Bragg' meachings that were mock-infected 48 hours prior to harvest. Dr. Gary Stacey generously donated the tissue. The roots were flash-frozen in liquid nitrogen. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (V=A, C, or G) was added to the 3' end of the primer (GAGAGAGAGAGAGAACTAGTCTCGAG(T)18V) to anchor the primer at the 5' end of the poly(A) tract. After second-strand synthesis, the cDNA ends were filled in with cloned Pfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The cDNA was then precipitated and redissolved in sterile, RNase-, DNase-free water. The XhoI site within the first- strand synthesis primer was then restricted by disgestion with XhoI from Promega (40V/ul); all XhoI sites in the CDNA constructs ware size-fractionated with a 500bp cutoff, using Sephacryl size-fractionated with a 500bp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately Init RCH) and phosphorylated, redissolved, and ligated into Stratagene's pBluescript II XR Predigested vector (PBLUESCTIP II XK) vector that has been digaeted with RCNI and phosphorylated) with a spendigested with
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/db_xrefe"taxon:3847"
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/dev stage="7 days old"
/lab_nost="DH108"
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    McCann, R., Waterston, R. and Wilson, R.
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/cultivar="Bragg"
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//note="Vector: pBluescript II SK+; Site_I: EcoRI; Site_2: Xhoi; The mRNA was isolated from rootes of 7 day old "Bragg" seedlings that were mock-infected 48 hours prior to harvest. Dr. Gary Stacey generously donated the tissue. The roots were flash-frozen in liquid nitrogen. Stratagene's cDNA Synthesis Kit (catalog number 200401) was used to synthesize the cDNA. First-strand synthesis was performed with 5-methyl dCTP, hence the ligated cDNA was hemimethylated. A modification of Stratagene's first-strand synthesis primer was used. An 'anchor' nucleotide (VeA, C, or G) was added to the 3' end of the primer [GAGAGAGAGAGAACTACTGAG[7] 1891 to anchor the primer [GAGAGAGAGAGAACTACTGAG[7] 1891 to anchor the primer at the 5' end of the cDNA ends were filled in with cloned bfu DNA, ligated to EcoRI adapters and subsequently phosphorylated. The cDNA was then precipitated and rediscolved in sterile, RNASe-', DNASe-free water. The XhoI site within the first- strand synthesis primer was then restricted by disestion with XhoI from Promega (400/ul); all XhoI sites in the cDNA constructs were hemimethylated status. The cDNA constructs were size-fractionated with a 500bp cutoff, using Sephacryl S-500 High Resolution (Pharmacia Biotech) in a 2-mm diameter column and a bed volume of approximately Iml. The column eluent was precipitated, redissolved, and ligated into Stratagene's pBluescript II XR Predigested vector (pBluescript II SK(+) vector that has been diagested with EcoRI and XhoI, and phosphorylated by Stratagene'). This library was constucted in the laboratory of Dr. Paul Keim and Dr. Virginia H. Coryell at Northern Arizona
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//clssue type="Roots of 7 day old 'Bragg' seedlings"
//dev_stage="7 days old"
//ab_host="DH108"
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/db_xref="taxon:3847"
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Best Local Similarity 48.83
Matches 278; Conservative
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/clone lib="Gm-c1051"
//once="Vector: pBluescript II SK+; Site 1: EcoR1; Site_2: ...
//once="Vector: pBluescript II SK+; Site 1: EcoR1; Site_2: ...
Xho1; The CDNA library was constructed from floral meristematic mRNA lorovided by Dr. Halina Knap of Clemson University. Complementary DNA was synthesized from mRNA using a primer consisting of a poly(dT) sequence with a XhoI restriction site. EcoRI adapters were ligated to the blunt-ended cDNA fragments followed by XhoI digestion. The CDNA fragments were directionally cloned into the EcoRI-XhoI restriction site of the pBluescript vector. The ligated cDNA fragments were transformed into DH10B host cells (GibcOSRE). This library was constructed in the laboratory of Dr. Randy Shoemaker."
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When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 424.
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Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Schurk, R., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
McCann, R., Waterston, R. and Wilson, R., Jackson, Y., Cardenas, M.,
Public Soybean EST Project
Unpublished (1999)
9709 CUCACCGACAUGAGUUUGGCGCGAUAUGCUUUUGAUUUCUAUGAAAUGACAUCAAGGACG 9768
                                                                                                                                                             9769 CCAGCUCGGGCCCGGGAAGCCCACAUCCAGAUGAAAGCUGCAGCAUUGCGAGAUGCGAAU 9828
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BF423777 541 bp mRNA linear EST 13-JUL-2004 8r38h04.yl Gm-c1051 Glycine max cDNA clone GENOME SYSTEMS CLONE ID: Gm-c1051-368 5' similar to SW:POLG SBMVN P21231 GENOME POLYPROTEIN [CONTAINS: NUCLEAR INCLUSION PROTEIN B ;, mRNA sequence.
                                                                                                                                                                                                                    Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                          Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
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| Organism="Glycine max"
| organism="Glycine max"
| cullivar="Corolla"
| db xref="taxon:3847"
| clone="GENOME SYSTEMS CLONE ID: Gm-c1051-368"
| clisue type="floral meristematic mRNA"
| lab_host="DH108"
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541 AACAAGTTGTTTGGACTTGATGGGAACATC 570
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1. Cosses 1 to 4.2).

Nascimento, L.U., Schutz, K., Matero, A., Swaby, I., See, L.-H.,

Nascimento, L.U., Schutz, K., Matero, A., Swaby, I., See, L.-H.,

Preston, R.R., Rodriguez, M.A., Shah, R.S., Shekher, M., Splegel, L.A.,

Vill, M.D., Dedhia, N.N. and McCombie, W.R.

Expressed sequence tags from Zea mays (maize)

Unpublished (2000)

Londate: W. Richard McCombie

Lita Annenberg Hazen Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 884

Fax: 516 367 884

Fax: 516 367 884

Email: mccombie@cshl.org

Plate: 2a69 row: h column: 07

Seq primer: -40M13ForUniv

High quality sequence stop: 475.
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                                                                                                                                                                                    9525 UAAUGGCAUGUGGUUUAUGAUGCAAGGGGAAGAACAAAUCGAAUACCCCCUUCAACCAAU 9584
                                                                                                                                                                                                                                               9585 AGUGGAAAACGCAAAACCCACUUUGCGUCAGAUUAUGGCUCACUUUAGCAAUGUUGCUGA 9644
                                                                                                                                                                                                                                                                                                         9645 AGCAUACAUCGAAAAGAGAAAUUAUGAGAAGCCAUAUAUGCCGAGGUACGGUAUUCAACG 9704
                                                                                                                                                                                                                                                                                                                                                                     9705 GAACCUCACCGACAUGAGUUUGGCGCGAUAUGCUUUUGAUUUCUAUGAAAUGACAUCAAG 9764
                                                                                                                                                                                                                                                                                                                                                                                                                               9765 GACGCCAGCUCGGGCCCGGGAAGCCCACAUCCAGAUGAAAGCUGCAGCAUUGCGAGAUGC 9824
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(bases 1 to 475)
                                                                                            9
                                                                               241 AGCTTACATTGAGATGAGAAATTCTGAAAGTCCGTATATGCCTAGATATGGACTACTACAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                 361 AACACCAAACAGGCAAGGAAGCAATAGCGCAGATGAAGGCTGCAGCTCTTTCGGGAGT
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                                    Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  481 GCACACTGCAAGGGATGTGAATCANAACATGCACACTCTNTTGGGCATGGGCT 533
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      541;
 2.4%; Score 246.8; DB 2; Length 50.3%; Pred. No. 6.7e-48; ive 85; Mismatches 180; Indels
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Query Match
Best Local Similarity 50.3 Matches 268; Conservative
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Choases 1 to 522)
Shoemaker,R., Keim,P., Vodkin,L., Erpelding,J., Coryell,V.,
Shoemaker,R., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Khanna,A., Bolla,B., Marra,M., Hillier,L., Kucaba,T., Martin,J.,
Beck,C., Wylie,T., Undervood,K., Steptoe,M., Theising,B., Allen,M.,
Bowers,Y., Person,B., Swaller,T., Gibbons,M., Pape,D., Harvey,N.,
Schurk,R., Ritter,E., Kohn,S., Shin,T., Jackson,Y., Cardenas,M.,
McCann,R., Waterston,R. and Wilson,R.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUUGGCGGAAAGGUUUGCGUCGAUGAUUUCAACAACCAAUUUUAUGAUGUUAAUAUGAAA 8154
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8155 UGCCCAUGGACAGUCGGGAUGACUAAGUUUUAUUGCGGAUGGAAUGAUCUUCUAGGUAAA 8214
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        247
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             427
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
rosids, eurosids I, Fabales, Fabaceae, Papilionoideae, Phaseoleae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  67
                                                                                                                                      /note="Vector: Lambda Zap II (Stratagene); Site_1: XhoI; Site_2: EcoRI; Resistance: Amploid1lln; Autoexcision: pBluescript SK (+/-); Titer: 7 x 10e-9 pfu/mL (as of 9/28/94); Library source: John Doebley, B73"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             248 CCTTATTTGATAAATGCAGTGCTTAATATTCGATTACAATTCATGGAACCATGGAATATT
                                                                                                                                                                                                                                                                                                                                                                                                                                                           CCAUACTUGCUGAAUGCAGUGCUCGGGAUTUAGGGAGUUUUUCAUGGAAGAUUGGGACAUA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            368 GATGGATCGTTATCAAGAAGTTTAAAGGTAATAACAGGGGACAGCCGTCAACAGTTGTT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CUUCCUGAUGGUUGGAUAUACCGCGAUGCUGACGGAUCACGAUUUGACAGUUCUCUUACA
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                                                                                                                                                                                                                                                                                                              Length 475;
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                                                                                                               CDNAs Library"
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                                                                                                                                                                                                                                                                                                                 DB 2;
                                                                                                                                                                                                                                                                                                                 h 2.4%; Score 246.6; DB 2 Similarity 51.2%; Pred. No. 7.2e-48;
                                                                               /clone="za69h07"
/clone lib="Maize Glume
/organism="Zea mays"
/mol_type="mRNA"
/db_xref="taxon:4577"
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/done_lib="Gm-c1051"
//note="Vector: pBluescript II SK+; Site 1: EcoRI; Site_2:
Xhof; The cDNA library was constructed from floral
meristematic mRNA provided by Dr. Halina Knap of Clemson
University. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
xhoI restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
cDNA fragments were directionally cloned into the
ECORI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into bHi0B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
77006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 414.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Glycine.

1 (bases 1 to 516)
Shoemaker, K. Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Shoemaker, Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
Public Soybean EST Project
Unpublished (1999)
                                                                                                                                                                                                 BG725155
sea33a07.y1 Gm-c1051 Glycine max CDNA clone GENOME SYSTEMS CLONE
1D1: Gm-c1051-6925 5' similar to SW:POLG SEMON P21231 GENOWE
POLYPROTEIN [CONTAINS: NUCLEAR INCLUSION PROTEIN B ;, mRNA
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Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1051-6925"
/tissue_type="floral meristematic mRNA"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ö
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                                               520
            86; Mismatches 171;
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/mol_type="mRNA"
/cultivar="Corolla"
                                                                                                                                                                                                                                                                                                                                                                                      BG725155.1 GI:14008551
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Matches 258; Conservative
                                                                                                                                                                                                                                                                                                                                sequence.
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Xho1; The CDNA library was constructed from floral
meristematic mRNA provided by Dr. Halina Knap of Clemson
University. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
Xho1 restriction site. EcoRl adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
CDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into bhe
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."
Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1800
Fax: 314 286 1810
Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTs on clone' field. This clone is available through: Blogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 415.
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'mol type="mRNA"
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Matches 267; Conservative
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Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J.,
Beck, C., Wyle, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Watter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
McCan, R., Wattersten, R. and Wilson, R.
Unpublished (1999)
Contact: Shoemaker R/Public Soybean EST Project
Washington University School of Medicine
4444 Forset Park Parkway, Box 8501, St. Louis, MO 63108, USA
Tel: 314 286 1810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Email: estewatson.wustl.edu
When it has been determined, an EST from the other end of this
volone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (Phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 359.
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                                    61 GCAGTTAAAGATGAATATGAGCTTGACGATGAGCAGATGGGTGTGGTTATGAATGGTTTC 120
                                                                                            181 GATGGAGAGGAACAGATTGAATATCCGCTGAAAACCCATTGTCGAAAAATGCAAAAACCTAAAAA
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GCUGUGAAGGAAUCCUAUGGUGUGUCUGAUGAAGAAAUGGGAAUAAUUUUGAAUGGAUUA
                                                                         AUGGUUUGGUGUAUUGAAAAUGGAACAUCUCCAAACAUUAAUGGCAUGUGGUUUAUGAUG
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VERSION
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/organism="Glycine max"

source

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/note="Vector: palescript II SK+; Site I: EcoRI; Site_2:
XhoI; The cDNA library was constructed from floral
meristenatic mRNA provided by Dr. Halina Knap of Clemson
University. Complementary DNA was synthesized from mRNA
using a primer consisting of a poly(dT) sequence with a
XhoI restriction site. EcoRI adapters were ligated to the
blunt-ended cDNA fragments followed by XhoI digestion. The
CDNA fragments were directionally cloned into the
EcoRI-XhoI restriction site of the pBluescript vector. The
ligated cDNA fragments were transformed into DH10B host
cells (GibcoBRL). This library was constructed in the
laboratory of Dr. Randy Shoemaker."
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  Gm-c1051-29"
: mRNA"
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/clone="GENOME SYSTEMS CLONE ID: G/tissue_type="floral meristematic
                                                                            clone lib="Gm-c1051"
                                                   lab_host="DH10B"
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/tissue type="glume ear 2 weeks post-pollination"
/cell_line="W22-TGA"
/cell_line="W22-TGA"
/cell_line="W22-TGA"
/note="Vector: pBLUGSCRIPT SK+ (X52325); Site 1: Xho!;
Site 2: ECORI; This library was supplied by John Doebley
(Univ. of Minnesota). cDNAs are directionally cloned into
the XhoI and ECORI sites; XhoI is near the polyA tail.
MOST reads from this library are made with the reverse
universal M13 primer and are 5' in direction. Additional
information on this library as well as ftp access to all
                                                                                                                                                                                                                                                                9786
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                                                                                      1667 UAUGAGAAGCCAUAUAUGCCGAGGUACGGUAUUCAACGGAACCUCACCGACAUGAGUUUG 9726
                                                                                                                                                                                                                                                                                                                       301 GCCCGCTATGATTTCTATGAGGTTACTTCCAAAACACCCAAAGGGAA 360
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                                                                                                                                         421 GATGGGAACATCTCAACTAACTCCGAAAATACTGAAAGGCACACTGCAAGGGATGTGAAT 480
         181 CTGAGACAAATTATGCACCACTTCTCAGATGCAGCAGAAGCTTACATTGAGATGAGAAAT 240
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACCAD
clade; Panicoideae; Andropogoneae; Zea.
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Norris,A., Parnell,L.D., Schutz,K., de la Bastide,M.,
Nascimento,L., Shah,R., Swaby,I., Shekher,M., Vil,M.D.,
Huang,E.N., Habermann,K., Dedhia,N., Martienssen,R. and
McCombie,W.R.
Expressed sequence tags from Z. mays (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Unpublished (1999)
Contact: W. Richard McCombie
Lita Annenberg Hazen Genome Sequencing Center
Cold Spring Harbor Laboratory
PO Box 100, Cold Spring Harbor, NY 11724, USA
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Seg primer: M13 reverse universal
High quality sequence stop: 461.
Location/Qualifiers
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/mol_type="mRNA"
/db_xref="taxon:4577"
/clone="au02c06"
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Fax: 516 367 8874
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AI372192
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Fax: 314 286 1800
When it has been determined, an EST from the other end of this clone is listed in the 'Other ESTB on clone' field. This clone is available through: Biogenetic Services, 801 32nd Ave. Brookings, SD 57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com) Seq primer: 40RP from Gibco
High quality sequence stope, 421.
                                                                                                                                                                                                                                                                                                                                                                                                                       J. Chaers. T. Coll., Solution of the Coll. V., Schoemaker. R., Keim. P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, B., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R. Unpublished (1999) Unpublished (1999) Unpublished (1999) Est Project Contact: Shoemaker R/Public Soybean EST Project Washington University School of Medicine Washington University School of Medicine Contact: Description of Medicine Collections of the Collection of Medicine Collections of the Collection of Medicine Collections of Collections o
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
rosids; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
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    BI320765.1 GI:14999951
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Best Local Similarity 51.5'
Matches 253; Conservative
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Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V.,
Khanna, A., Bolla, B., Marra, M., Hiller, L., Kucaba, T., Martin, J.,
Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M.,
Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N.,
Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M.,
MCGann, R., Waterston, R. and Wilson, R.
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  /clone_lib="Maize Glume cDNAs Library"
/note="Vector: Lambda Zap II (Stratagene); Site_1: XhoI;
Site_2: EcoRI; Resistance: Ampicillin, Autoexcision:
pBluescript SK (+/-); Titer: 7 x 10e-9 pfu/mL (as of
9/28/94); Library source: John Doebley, B73"
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                                                                                                                                                                                                                                                                                                                                                    GAAAUGGGAAUAAUUUUGAAUGGAUUAAUGGUUUGGUGUAUUGAAAAUGGAACAUCUCCA
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Public Soybean EST Project
Washington University School of Medicine
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                   DB 2; Length 470;
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                                                                                                                                                                Ouery Match 2.3%; Score 231.6; DB 2; Length Best Local Similarity 51.3%; Pred. No. 3e-44; Matches 241; Conservative 80; Mismatches 149; Indels
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(1 bases 1 to 4).

(2 C. Shaughnessy, A. L., Habermann, K., de la Bastide, M., Huang, E. N., Nascimento, L. U., Schutz, K., Matero, A., Swaby, I., See, L. H., Vil, M. D., Dedhia, N. N. and McCombie, W. R.

Expressed sequence tags from Zea mays (maize)

Unpublished (2000)

Contact: W. Richard McCombie
Lita Annenberg Haren Genome Sequencing Center

Cold Spring Harbor Laboratory

PO Box 100, Cold Spring Harbor, NY 11724, USA

Tel: 516 367 8874
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za86hl0.g52 Maize Glume cDNAs Library Zea mays cDNA clone za86hl0
BE051689
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        8420 GAGGAAAUAAUAGUGGUCAACCGUCAACAGUCGUAGAUAACACAUUGAUGGUCUGUAUUU 8479
                                                                                                                                                                                                                                                                                                         300
                                                                                                                                                                                                                61 ATTITAATAATCAATTCTATTCACATCATTTAGAAGGTCCATGGACTGTTGGAATAACAA 120
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                                                                                                                   CTCGAACCTTCACAGCAGCCCCATTAGAGACTTTACTCGGAGGAAAAGTGTGGCGTAGATG
                                                                                                                                                                                                                                                                                                                                                                                                    181 ATGCTGACGGATCTCAATTTGATAGTTCATTAACACCATATCTCATCAATGCAGTATTAA
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                                                                                             8060 CGCGAACAUUCACAGCAGCUCCAAUUGAAACUUUACUUGGCGGAAAGGUUUGCGUCGAUG
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; Score 231.6; DB 1;
; Pred. No. 3e-44;
91; Mismatches 139;
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High quality sequence stop: 470.
Location/Qualifiers
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Plate: za86 row: h column: 10
Seg primer: -40M13RevUniv
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/db_xref="taxon:4577"
/clone="za86h10"
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/organism="Zea mays"
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    2.3%;
Query Match
Best Local Similarity 49.3#
Matches 224; Conservative
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Zea mays Zea mays

ORGANISM

REFERENCE AUTHORS

TITLE JOURNAL COMMENT

source

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KEYWORDS

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RESULT 13 BE051689

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mRNA sequence.
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//mol type="mRNA"
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//clone="centorial meristematic mRNA"
//clone="centorial meristematic mRNA"
//clone="centorial meristematic mRNA"
//lab host="blubilog"
//lab host="centorial host blubilog host cells (Gibcorial host)
//lab host cells library was constructed in the laboratory of Dr. Randy Shoemaker."
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                               Email: est@watson.wustl.edu
When it has been determined, an EST from the other end of this
clone is listed in the 'Other ESTs on clone' field. This clone is
available through: Biogenetic Services, 801 32nd Ave. Brookings, SD
57006 USA (phone: 800 423 4163; email: info@biogeneticservices.com)
High quality sequence stop: 394.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9468 AAUAAUJUUGAAUGGAUUAAUGGUUUGGUGUAUUGAAAAUGGAACAUCUCCAAACAUUAA 9527
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 308 CGAAAATGCAAAACCAACTTTGAGACAAAATTATGCACCATTTCTCAGATGCAGCAGAAGC 367
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                                                                                                                                                                                                               /organism="Glycine max"
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Best Local Similarity 48.2*
Matches 248; Conservative
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/clone ltb="Gm-ri070"
/rote="Trbe library Gm-ri070"
/rote libraries from mimature cotyledons, l.770
from immature seed coats, 3.938 from flowers, and 869
from immature seed coats, 3.938 from flowers, and 869
from young pods. Trbe 5. ESTS of the source clones from
the different libraries was used to select singletons, or
a representative of each contig, which were reracked to
form library Gm-ri070. The cDNA clones of the reracked
Gm-ri070 library Gm-ri070. The cDNA clones of the reracked
contig analysis to select unique genes was performed by
the laboratory of Ernest Retzel, Center for Computational
Genomics and Bioinformatics, University of Minnesota,
http://www.genomesystems.com, and 3' sequencing by the
Keck Center for Comparative and Functional Genomics,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 University of Illinois, http://www.life.uiuc.edu/biotech/keck.html. Note: The corresponding 5' EST from each clone in the Gm-I070 library is listed in the 'OTHER EST' field. The detailed information on the source library for each clone can also be obtained by referring to the Genome Systems clone ID of the original cDNA library that is also listed under 'OTHER EST'."
BE820764 1758 bp mRNA linear EST 24-MAY-2001 GM700012A20H1 Gm-r1070 Glycine max cDNA clone Gm-r1070-4946 3'',
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Other ESTS: AW459391 corresponding to Gm-c1016-5630 (5')
Contact: Vodkin, L.O., PI, A Functional Genomics Program for Soybean (NSF 9872565)
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49.5%; Pred. No. 1.2e-43;
tive 80; Mismatches 177;
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/organism="Glycine max"
/mol_type="mRNA"
/db_xref="texon:3847"
/clone="Gm-r1070-4946"
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Glycine max
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Best Local Similarity 49.53
Matches 252; Conservative
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9424 AACGCUGUGAAGGAAUCCUAUGGUGUCUGAUGAAGAAAUGGGAAUAAUUUUGAAUGGA 9483
                                                                                                                                AAUUAUGAGAAGCCAUAUAUGCCGAGGUACGGUAUUCAACGGAACCUCACCGACAUGAGU 9723
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                                                                                               ACUUUGCGUCAGAUUAUGGCUCACUUUAGCAAUGUUGCUGAAGCAUACAUCGAAAAGAGA
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Search completed: September 5, 2005, 10:23:42 Job time : 27846 secs